

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 22, 2004, 08:59:04 ; Search time 48 Seconds
(without alignments)

2576.112 Million cell updates/sec

Title: US-09-983-000A-20

Perfect score: 2342

Sequence: 1 MRTLPLPALLTCWLLAPVNS.....LQPHGRSAQSLQTETSVI 438

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2342	100.0	438	10	US-09-983-000A-20
2	2327	99.4	438	14	US-10-157-031-237
3	2327	99.4	438	14	US-10-225-567A-471
4	2321	99.1	438	11	US-09-826-509-581
5	1153.5	49.3	467	9	US-09-935-371-19
6	1151.5	49.2	485	9	US-09-935-371-17
7	1150	49.1	468	15	US-10-292-798-638
8	1150	49.1	525	9	US-09-935-371-23
9	1150	49.1	525	13	US-10-044-722-3
10	1150	49.1	525	15	US-10-225-567A-231
11	1150	49.1	525	15	US-10-295-027-276
12	1144.5	48.9	468	11	US-09-935-371-22
13	1144	48.8	468	11	US-09-826-509-553
14	1143.5	48.8	448	9	US-09-935-371-18
15	1141.5	48.7	448	9	US-09-935-371-16
					Sequence 20, Appl
					Sequence 237, App
					Sequence 471, App
					Sequence 581, App
					Sequence 19, Appl
					Sequence 17, Appl
					Sequence 638, App
					Sequence 23, Appl
					Sequence 3, Appl
					Sequence 231, App
					Sequence 276, App
					Sequence 22, Appl
					Sequence 553, App
					Sequence 18, Appl
					Sequence 16, Appl

16	1129.5	48.2	495	9	US-09-935-371-21	Sequence 21, Appl
17	1127.5	48.1	513	9	US-09-935-371-15	Sequence 15, Appl
18	1126.5	48.1	552	9	US-09-935-371-27	Sequence 27, Appl
19	1126	48.1	553	9	US-09-935-371-25	Sequence 25, Appl
20	1126	48.1	553	9	US-09-935-371-29	Sequence 29, Appl
21	1121	47.9	475	9	US-09-935-371-26	Sequence 26, Appl
22	1120.5	47.8	476	9	US-09-935-371-24	Sequence 24, Appl
23	1120.5	47.8	476	9	US-09-935-371-28	Sequence 28, Appl
24	1119.5	47.8	476	9	US-09-935-371-20	Sequence 20, Appl
25	1117.5	47.7	476	9	US-09-935-371-14	Sequence 14, Appl
26	1064.5	45.5	1324	9	US-09-935-371-56	Sequence 56, Appl
27	1035.5	44.2	457	14	US-10-225-567A-469	Sequence 469, App
28	1035.5	44.2	457	15	US-10-292-798-618	Sequence 618, App
29	1029.5	44.0	457	11	US-09-826-509-579	Sequence 579, App
30	1018	43.5	495	15	US-10-295-027-875	Sequence 875, App
31	1004.5	42.9	440	14	US-10-225-567A-310	Sequence 310, App
32	1003.5	42.8	440	12	US-10-398-454-3	Sequence 3, Appli
33	1003.5	42.8	440	12	US-10-398-455-3	Sequence 2, Appli
34	1003.5	42.8	440	15	US-10-292-798-608	Sequence 608, App
35	1003.5	42.8	440	15	US-10-051-874-64	Sequence 64, Appl
36	1003.5	42.8	440	16	US-10-051-874-65	Sequence 65, Appl
37	1003.5	42.8	440	16	US-10-398-448-3	Sequence 3, Appli
38	998.5	42.6	440	11	US-09-826-509-567	Sequence 567, App
39	997.5	42.6	440	15	US-10-051-874-66	Sequence 66, Appl
40	997.5	42.6	449	15	US-10-051-874-68	Sequence 68, Appl
41	992.5	42.4	440	15	US-10-051-874-67	Sequence 67, Appl
42	980.5	41.9	421	15	US-10-051-874-10	Sequence 10, Appl
43	881.5	37.6	423	15	US-10-292-798-640	Sequence 640, App
44	879.5	37.6	423	14	US-10-147-087-4	Sequence 4, Appli
45	879.5	37.6	423	14	US-10-225-567A-142	Sequence 142, App

ALIGNMENTS

RESULT 1

US-09-983-000A-20
; Sequence 20, Application US/09983000A
; Publication No. US20030118585A1

GENERAL INFORMATION:
; APPLICANT: AGY Therapeutics

; APPLICANT: Melcher, Thorsten

; APPLICANT: Mueller, Sabine

; APPLICANT: Chin, Daniel

; TITLE OF INVENTION: USE OF PROTEIN BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUALIZ

; TITLE OF INVENTION: OF BRAIN TUMORS

; FILE REFERENCE: 263/180 -- Peagleman -- AGY

; CURRENT FILING DATE: 2001-10-17

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: Patent version 3.1

; SEQ ID NO 20

; LENGTH: 438

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: (1)..(23)

; OTHER INFORMATION: Potential

; NAME/KEY: GENE

; LOCATION: (1)..(438)

; OTHER INFORMATION: Vasoactive Intestinal Peptide Receptor 2

; NAME/KEY: CHAIN

; LOCATION: (24)..(438)

; OTHER INFORMATION: Vasoactive Intestinal Polypeptide Receptor 2

; NAME/KEY: DOMAIN

; LOCATION: (24)..(126)

; OTHER INFORMATION: 1 (Potential)

; NAME/KEY: TRANSMEM

; LOCATION: (127)..(151)

; OTHER INFORMATION: 1 (Potential)

; NAME/KEY: DOMAIN

; LOCATION: (152)..(158)

OTHER INFORMATION: Cytoplasmic (potential)
 NAME/KEY: TRANSMEM
 LOCATION: (159)..(178)
 OTHER INFORMATION: 2 (Potential)
 NAME/KEY: DOMAIN
 LOCATION: (179)..(203)
 OTHER INFORMATION: Extracellular (Potential)
 NAME/KEY: TRANSMEM
 LOCATION: (204)..(227)
 OTHER INFORMATION: 3 (Potential)
 NAME/KEY: DOMAIN
 LOCATION: (228)..(240)
 OTHER INFORMATION: Cytoplasmic (Potential)
 NAME/KEY: TRANSMEM
 LOCATION: (241)..(262)
 OTHER INFORMATION: 4 (Potential)
 NAME/KEY: DOMAIN
 LOCATION: (263)..(279)
 OTHER INFORMATION: Extracellular (Potential)
 NAME/KEY: TRANSMEM
 LOCATION: (280)..(303)
 OTHER INFORMATION: 5 (Potential)
 NAME/KEY: DOMAIN
 LOCATION: (304)..(328)
 OTHER INFORMATION: Cytoplasmic (Potential)
 NAME/KEY: TRANSMEM
 LOCATION: (329)..(348)
 OTHER INFORMATION: 6 (Potential)
 NAME/KEY: DOMAIN
 LOCATION: (349)..(360)
 OTHER INFORMATION: Extracellular (Potential)
 NAME/KEY: TRANSMEM
 LOCATION: (361)..(380)
 OTHER INFORMATION: 7 (Potential)
 NAME/KEY: DOMAIN
 LOCATION: (381)..(438)
 OTHER INFORMATION: Cytoplasmic (potential)
 NAME/KEY: CARBOHYD
 LOCATION: (58)..(58)
 OTHER INFORMATION: N-linked (GLCNAC...) (Potential)
 NAME/KEY: CARBOHYD
 LOCATION: (88)..(88)
 OTHER INFORMATION: N-linked (GLCNAC...) (Potential)
 NAME/KEY: CARBOHYD
 LOCATION: (92)..(92)
 OTHER INFORMATION: N-linked (GLCNAC...) (Potential)

US-09-983-000A-20

Query Match
 Best Local Similarity 100.0%; Score 2342; DB 10; Length 438;
 Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELRSQTEKHKACSGVWDNIT 60
 DB 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELRSQTEKHKACSGVWDNIT 60

QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120
 DB 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120

QY 121 TFYILVKAIYTLGYSVLSLMSLATGSIILCLPRKLHCTRNYIHLNLFSLFIRALSVLVKD 180
 DB 121 TFYILVKAIYTLGYSVLSLMSLATGSIILCLPRKLHCTRNYIHLNLFSLFIRALSVLVKD 180

QY 181 DVLXSSGTLHCPDPSPSSWVGCKLSLVFLQYICIMANFWLLVEGLYHHTLVAMLPERRC 240
 DB 181 DVLXSSGTLHCPDPSPSSWVGCKLSLVFLQYICIMANFWLLVEGLYHHTLVAMLPERRC 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIIYNFVLF 300
 DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIIYNFVLF 300

QY 301 SIIRILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQLIFE 360
 DB 301 SIIRILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQLIFE 360

QY 361 LCLGSFQGLVAVLYCFINSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGALQ 420
 DB 361 LCLGSFQGLVAVLYCFINSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGALQ 420

Db 301 SIIRILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQLIFE 360
 QY 361 LCLGSFQGLVAVLYCFINSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGALQ 420
 Db 361 LCLGSFQGLVAVLYCFINSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGALQ 420
 QY 421 FHRGSAQSFLOTETSVI 438
 Db 421 FHRGSAQSFLOTETSVI 438

RESULT 2

US-10-157-031-237
 ; Sequence 237, Application US/10157031
 ; Publication No. US20030108890A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baranova, A. V.
 ; APPLICANT: Yankovsky, N. K.
 ; APPLICANT: Kozlov, A. P.
 ; APPLICANT: Lobashev, A. V.
 ; APPLICANT: Krukovskaya, L. L.
 ; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
 ; FILE REFERENCE: 2760-103
 ; CURRENT APPLICATION NUMBER: US/10/157,031
 ; NUMBER OF SEQ ID NOS: 415
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 237
 ; LENGTH: 438
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-157-031-237

Query Match
 Best Local Similarity 99.4%; Score 2327; DB 14; Length 438;
 Matches 435; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELRSQTEKHKACSGVWDNIT 60
 DB 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELRSQTEKHKACSGVWDNIT 60

QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120
 DB 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120

QY 121 TFYILVKAIYTLGYSVLSLMSLATGSIILCLPRKLHCTRNYIHLNLFSLFIRALSVLVKD 180
 DB 121 TFYILVKAIYTLGYSVLSLMSLATGSIILCLPRKLHCTRNYIHLNLFSLFIRALSVLVKD 180

QY 181 DVLXSSGTLHCPDPSPSSWVGCKLSLVFLQYICIMANFWLLVEGLYHHTLVAMLPERRC 240
 DB 181 DVLXSSGTLHCPDPSPSSWVGCKLSLVFLQYICIMANFWLLVEGLYHHTLVAMLPERRC 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIIYNFVLF 300
 DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIIYNFVLF 300

QY 301 SIIRILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQLIFE 360
 DB 301 SIIRILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQLIFE 360

QY 361 LCLGSFQGLVAVLYCFINSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGALQ 420
 DB 361 LCLGSFQGLVAVLYCFINSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGALQ 420

QY 421 FHRGSAQSFLOTETSVI 438
 DB 421 FHRGSAQSFLOTETSVI 438

RESULT 3

US-10-225-567A-471

```
; Sequence 471, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2392
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 471
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-225-567A-471

Query Match          99.4%; Score 2327; DB 14; Length 438;
Best Local Similarity 99.3%; Pred. No. 7.3e-216;
Matches 435; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPCRFHLIEQEEETKCAELLRSQTEKHKACSGWVDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPCRFHLIEQEEETKCTELLRSQTEKHKACSGWVDNIT 60
QY 61 CWRPANVGETVTVPCKVFNFSKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120
Db 61 CWRPANVGETVTVPCKVFNFSKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120
QY 121 TFYLKAIYTLGYSVLSLMSLATGSIILCLFRKLHCTRNVIHLNLFSLFIRALISVLVKD 180
Db 121 TFYLKAIYTLGYSVLSLMSLATGSIILCLFRKLHCTRNVIHLNLFSLFIRALISVLVKD 180
QY 181 DVLYSSGTLHCPDQSSWGCKLSLVFLOYCYIMANFFWLLVEGLYHLTLVAMLPERRC 240
Db 181 DVLYSSGTLHCPDQSSWGCKLSLVFLOYCYIMANFFWLLVEGLYHLTLVAMLPERRC 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCWDNDHSVPWWIRIPILISIIIVNFVLF 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCWDNDHSVPWWIRIPILISIIIVNFVLF 300
QY 301 SIIRILLQKLTSPDVGNDSQYKRLAKSTLLILPLFGVHYMVFAVFPPISSIKYQLFE 360
Db 301 SIIRILLQKLTSPDVGNDSQYKRLAKSTLLILPLFGVHYMVFAVFPPISSIKYQLFE 360
QY 361 LCLGSFQGLVAVLYCFLNSEVOCELKRWRCPTPSASRDYRVCGSSFRNGSEGLQ 420
Db 361 LCLGSFQGLVAVLYCFLNSEVOCELKRWRCPTPSASRDYRVCGSSFRNGSEGLQ 420
QY 421 FHRGSAQSFLOTETSVI 438
Db 421 FHRASRAQSFLOTETSVI 438

RESULT 4
US-09-826-509-581
; Sequence 581, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
```

```
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 581
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-826-509-581

Query Match          99.1%; Score 2321; DB 11; Length 438;
Best Local Similarity 99.1%; Pred. No. 2.8e-215;
Matches 434; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPCRFHLIEQEEETKCAELLRSQTEKHKACSGWVDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPCRFHLIEQEEETKCTELLRSQTEKHKACSGWVDNIT 60
QY 61 CWRPANVGETVTVPCKVFNFSKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120
Db 61 CWRPANVGETVTVPCKVFNFSKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120
QY 121 TFYLKAIYTLGYSVLSLMSLATGSIILCLFRKLHCTRNVIHLNLFSLFIRALISVLVKD 180
Db 121 TFYLKAIYTLGYSVLSLMSLATGSIILCLFRKLHCTRNVIHLNLFSLFIRALISVLVKD 180
QY 181 DVLYSSGTLHCPDQSSWGCKLSLVFLOYCYIMANFFWLLVEGLYHLTLVAMLPERRC 240
Db 181 DVLYSSGTLHCPDQSSWGCKLSLVFLOYCYIMANFFWLLVEGLYHLTLVAMLPERRC 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCWDNDHSVPWWIRIPILISIIIVNFVLF 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCWDNDHSVPWWIRIPILISIIIVNFVLF 300
QY 301 SIIRILLQKLTSPDVGNDSQYKRLAKSTLLILPLFGVHYMVFAVFPPISSIKYQLFE 360
Db 301 SIIRILLQKLTSPDVGNDSQYKRLAKSTLLILPLFGVHYMVFAVFPPISSIKYQLFE 360
QY 361 LCLGSFQGLVAVLYCFLNSEVOCELKRWRCPTPSASRDYRVCGSSFRNGSEGLQ 420
Db 361 LCLGSFQGLVAVLYCFLNSEVOCELKRWRCPTPSASRDYRVCGSSFRNGSEGLQ 420
QY 421 FHRGSAQSFLOTETSVI 438
Db 421 FHRASRAQSFLOTETSVI 438

RESULT 5
US-09-935-371-19
; Sequence 19, Application US/09935371
; Patent No. US20020155533A1
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Masuda, Yasushi
; APPLICANT: Kitada, Chieko
; APPLICANT: Ishibashi, Yoshihiro
; APPLICANT: Hosoya, Masaki
; APPLICANT: Ogi, Kazuhiro
; APPLICANT: Miyamoto, Yasunori
; APPLICANT: Shimamoto, Yugo
; TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
```

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/935,371
; FILING DATE: 22-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,474
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-935-371-19

Query Match 49.3%; Score 1153.5; DB 9; Length 467;
Best Local Similarity 49.7%; Pred. No. 1.7e-102;
Matches 226; Conservative 63; Mismatches 127; Indels 39; Gaps 6;

QY 10 LTCWLLAPVNSIHPCEHFLEIQEBETKCAEL-----LRSQTEKHKACGVDNITCWR 63
Db 9 LTALLPVVAIAHSDCIF---KKGQAMCLEIKQIQRNDLMLGNDSSPGCGMWDNITCWK 64

QY 64 PANVGETVTPCPKVFNSF-----YSKAGNISKNCTSDGNS 100
Db 65 PAQGVEMVLVCPVEFRIFNPQVMTETIGDSGFADSNLSLEITDMGVVGRNCTEDGNS 124

QY 101 TFPDFVDAGGYS--PEDESKITFYILVKAIVTLGYSVLSMISLATSIIICLFRKLHCTR 158
Db 125 PPHFYFDAGFDYDPESGDQDYLYLVKALYTVGYSTSLATLTAMVILCRFLHCTR 184

QY 159 NYIHLNLFILRAISLVLDKDVLYSSSGTLCPCDPQSSWYGCKLSLVFLQYCIAMNPF 218
Db 185 NFHNNLFFVSMRLAISLVFKWILYAEQDSSHC---FVSTVECKAVWVFFHYCVVSNYP 241

QY 219 WLLVGLYIHTLLV-AMLPFRRCFLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDH 277
Db 242 WLFIEGLYLTLLVETFPFERYFYWYTIIGWGTPTVCVTVNAVLRLYPDDAGCDWMDNS 301

QY 278 SVPMWVIRIPILISIVNFVLFISIRILLQKLTSPDIVGNDQSQYKRLAKSTILLILPLF 337
Db 302 TALWVVKGPVGSIMVNFVLFISIRILLQKLTSPDIVGNDQSQYKRLAKSTILLILPLF 361

QY 338 GVHYMVFAVPIISISKYILFELCLGSPQGLVAVLYCFNLSEVQCELRKRWGRKCPPT 397
Db 362 GIHYTVFAFSPENVSKRELVELGLGSPQGFVAVLYCFNLSEVQCELRKRWGRKCPPT 421

QY 398 SASRIRYVCGSFSRNGSEGLAQFHGRSQAQFLQ 432
Db 422 YFTMDPKRHRPGLASSGVNGGTQLSLSKSSQLR 456

```

RESULT 6

```

US-09-935-371-17
; Sequence 17, Application US/09935371
; Patent No. US2002015533A1
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; OHTAKI, Tetsuya
; MASUDA, Yasuhiro

```

```

;
; KITADA, Chieko
; ISHIBASHI, Yoshihiro
; HOSoya, Masaki
; OGI, Kazuhiro
; MIYAMOTO, Yasunori
; HABATA, Yugo
; SHIMAMOTO, No. US2002015533A1
; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR PREPARING
; SAID PROTEIN, AND USE THEREOF
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; CUSHMAN
; STREET: 130 Water Street
; City: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/935,371
; FILING DATE: 22-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,474
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-935-371-17

```

```

Query Match 49.2%; Score 1151.5; DB 9; Length 485;
Best Local Similarity 48.6%; Pred. No. 2.8e-102;
Matches 224; Conservative 72; Mismatches 126; Indels 39; Gaps 6;

QY 1 MRTLPPALLTCWLLAPVNSIHPCEHFLEIQEBETKCAEL-----LRSQTEKHKACG 54
Db 18 MASTAQVSLAALLLPMTAMHSDCIF---KKGQAMCLEIKQIQRNDLMLGNDSSPGCGP 73

QY 55 VMDNITCWRPANVGSTVTPCPKVFNSF-----YSKAGNISK 91
Db 74 MWDNITCWRPANVGSTVTPCPKVFNSF-----YSKAGNISK 133

QY 92 NCTSDGSETPPDFVDAGGYSDEDES--KITFYILVKAIVTLGYSVLSMISLATSIIIC 149
Db 134 NCTEDGSEPPFPYFDAGGFEYSETDQDYLYLVKALYTVGYSTSLATLTAMVILC 193

QY 150 LFRKLHCTRNYIHLNLFILRAISLVLDKDVLYSSSGTLCPCDPQSSWYGCKLSLVFL 209
Db 194 RFRKLHCTRNYIHLNLFILRAISLVLDKDVLYSSSGTLCPCDPQSSWYGCKLSLVFL 250

QY 210 QYCIAMNFFWLLVGLYIHTLLV-AMLPFRRCFLAYLLIGWGLPTVCIGAWTAARLYLED 268
Db 251 HCVVSNFYFWLFIEGLYLTLLVETFPFERYFYWYTIIGWGTPTVCVTVNAVLRLYPDD 310

QY 269 TCGWDNDHNSVPMWVIRIPILISIVNFVLFISIRILLQKLTSPDIVGNDQSQYKRLAK 328
Db 311 TCGWDMDNDNTALWWVVKGPVGSIMVNFVLFISIRILLQKLTSPDIVGNDQSQYKRLAK 370

```


APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 276
LENGTH: 525
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-276

Query Match 49.1%; Score 1150; DB 15; Length 525;
Best Local Similarity 48.2%; Pred. No. 4.4e-102;
Matches 225; Conservative 68; Mismatches 118; Indels 56; Gaps 7;
12 CW-----LLAPVNSHPCRFHLEQBEETKCAELLRSQTE-----X 48
52 CWPRSVAGVVHVSIAALLLPAPAMHSDCIF----KKEQAMCLEKIQRANELMGFND 107
49 HKACSGVWDNITCWPRANVGTVTVPCKVFSNF-----YSK 85
108 SPGCPGMDNITCWKPAHVGEMVLVSCPELFRIENPQVWETETIGESDFGDSNLSLD 167
86 AGNISKNCTSDGSETFPDVFADAGYSDPEDES--KITFYILVKAIYTLGYSVLSMSIAT 143
168 MGVSVRNCTEDGWESEPFPHYFDACGDEYBSETGDQDYIYLSVKALYTVGSTSLVLT 227
144 GSIILCLFRKLHCTRNVIHLNLSFTILRAISLVKDDVLVSSGTHLCPDQPSWVGCK 203
228 AMVILCRFKLHCTRNFIHNLNLFVSFMLRAISVFIKDWILYAEQDSNHC---FISTVECK 284
204 LSLVFLQCYIMANPFWLLVGLYLHTLLV-AMLPFRRCFLAYLLIGWLPVCIQAWTAA 262
285 AVMVFFHYCVSVYFWLFIQGLYLFTLLVETFFPERRYFWYTIIGMTGTTCVTVWATL 344
263 RLYLEDTCGWDNDHSDVWVWIRIPILISIVNVLVFIIRILLOKLTSPDVGNDQSQ 322
345 RLXPDDTGCWDMNDSTALWVWIKGPVVGSIWNVFLVFIIVILVQKLQSPDMGNESSI 404
323 YKRLAKSTLLILPLFGVHYVWVFAVFPISISKYQILFELCLGSPQGLVAVLYCFINSEV 382
405 YLRJARSTLLILPLFGIHYTVFAFSPENVKRELVEFLGLGSPQGFVAVLYCFINSEV 464
383 QCELKRWKRCPTPSASRYRVCGSSFRNSGSEGALQPHRGSRAQS 429

Db 465 QAEIKRWKRWKVNRYPAVDFKRRHPSLASSGVNGGTQLSILSKSS 511
RESULT 12
US-09-935-371-22
Sequence 22, Application US/09935371
Patent No. US20020155533A1
GENERAL INFORMATION:
APPLICANT: ONDA, Haruo
OHTAKI, Tetsuya
MASUDA, Yasushi
KITADA, Chieko
ISHIBASHI, Yoshihiro
HOSOYA, Masaaki
OGI, Kazuhiro
MIYAMOTO, Yasunori
HABATA, Yugo
SHIMAMOTO, No. US20020155533A1
TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/935,371
FILING DATE: 22-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/201,474
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, David S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 44168-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-935-371-22

Query Match 48.9%; Score 1144.5; DB 9; Length 448;
Best Local Similarity 50.1%; Pred. No. 1.2e-101;
Matches 221; Conservative 67; Mismatches 114; Indels 39; Gaps 6;
QY 21 IHPECFHLEIQBEETKCAELLRSQTE-----XSKAGNISKNCTSDGSETFPDVFADAGY 111
Db 1 MHSDCIF----KKEQAMCLEKIQRANELMGFNDSPGCPGMDNITCWKPAHVGEMVLV 56
QY 75 CPKVFNSF-----XSKAGNISKNCTSDGSETFPDVFADAGY 111
Db 57 CPFLFRIFNPQVWETETIGESDFGDSNLSLDGMSVSRNCTEDGWSFPFPHYFDACGF 116
QY 112 SDPEDES--KITFYILVKAIYTLGYSVLSMSIATGSIILCLFRKLHCTRNVIHLNLSF 169
Db 117 DEYSETGDQDYIYLSVKALYTVGSTSLVLTAMVILCRFKLHCTRNFIHNLVFSF 176


```
Db 57 CPEVFRIFNPQVWMTETIGDSGFADNSLEITDMGVVGRNCTEDGWSEPPHYFDACGF 116
QY 112 SD--PEDESKITFYILVKAITYTGYSVLSLATSIIICLFRKLHCTRYIHLNLFSP 169
Db 117 DYPEGSDQDYLYSVKALYTVGYSTSLATLTAMVILCRFKLHCTRFIHMNLFVSF 176
QY 170 ILRAISVLVVDVLYSSSGTLHCPDQPSWVGCKLSLVFLQYCIAMNFFWLLVGLYLHT 229
Db 177 MLRAISVFIKDWILYAEQDSHC---FVSTVECKANVWFHYCVSVYFWLFIEGLYLT 233
QY 230 LLV-AMLPFRRCFIAYLLIGWGLPTVCIGAWTAARLYLEDTCWDTNDHSPVWVIRPI 288
Db 234 LLVETFPERRFYFYIICWGTPVTCVSVWAMLRLYFDDTGCDWMDNDSTALMWVKGVP 293
QY 289 LISIIVNVLFIISIRILLOKLTSPDVGNDQSOYKRLAKSTLLILPLFGVHMVFAVFP 348
Db 294 VGSIMWNFVLFIGIIVILVQKLOSPDMGNESSIYLRLARSTLLILPLFGIHYTVFAFSP 353
QY 349 ISISSKYQILFELCLGSFQGLVAVLYCFLNSEVQCEBKRWRSRCPTPSASRDYRVCGS 408
Db 354 ENVSKEERLVFELGLGSFQGVVAVLYCFLNGEVAQAEIKRWRSWKVNRFTWDFKRRHP 413
QY 409 SFRNGSEGALQPHRGSRAQSFLQ 432
Db 414 SLASSGVNGGTQLSILSKSSQLR 437
```

RESULT 15

US-09-935-371-16

; Sequence 16, Application US/09935371

; Patent No. US2002015533A1

; GENERAL INFORMATION:

; APPLICANT: ONDA, Haruo

; OHTAKI, Tetsuya

; MASUDA, Yasushi

; KITADA, Chieko

; ISHIBASHI, Yoshihiro

; HOSoya, Masaki

; OGI, Kazuhiro

; MIYAMOTO, Yasunori

; HABATA, Yugo

; SHIMAMOTO, No. US2002015533A110

; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR PREPARING

; SAID PROTEIN, AND USE THEREOF

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &

; CUSHMAN

; STREET: 130 Water Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: US

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/935,371

; FILING DATE: 22-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/201,474

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: RESNICK, David S.

; REGISTRATION NUMBER: 34235

; REFERENCE/DOCKET NUMBER: 44168-DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)523-3400

; TELEFAX: (617)523-6440

```
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-935-371-16
```

Query Match 48.7%; Score 1141.5; DB 9; Length 448;

Best Local Similarity 49.9%; Pred. No. 2.4e-101;

Matches 220; Conservative 68; Mismatches 114; Indels 39; Gaps 6;

```
QY 21 IHPECRPHLEIQEETKCAEL-----LRSQTEKHKACSGVNDNITCWRPANGETVTP 74
Db 1 MHSDCLF---KKEQAMCLEKIQRVNDLMGLNDSPPCGPWNDNITCWKPAHUGENVLVS 56
QY 75 CPKVFSNF-----YSKAGNISKNCTSDGWSSETFPDFVDACGY 111
Db 57 CPSELRIFRNPQVWMTETIGEGFADSKSLDLSMRVVSRNCTEDGWSEPPHYFDACGF 116
QY 112 SDPEDES--KITFYILVKAITYTGYSVLSLATSIIICLFRKLHCTRYIHLNLFSP 169
Db 117 EYSESETGDDQDYLYSVKALYTVGYSTSLVTLTAMVILCRFKLHCTRFIHMNLFVSF 176
QY 170 ILRAISVLVVDVLYSSSGTLHCPDQPSWVGCKLSLVFLQYCIAMNFFWLLVGLYLHT 229
Db 177 MLRAISVFIKDWILYAEQDSNHC---FVSTVECKANVWFHYCVSVYFWLFIEGLYLT 233
QY 230 LLV-AMLPFRRCFIAYLLIGWGLPTVCIGAWTAARLYLEDTCWDTNDHSPVWVIRPI 288
Db 234 LLVETFPERRFYFYIICWGTPVTCVSVWAMLRLYFDDTGCDWMDNDSTALMWVKGVP 293
QY 289 LISIIVNVLFIISIRILLOKLTSPDVGNDQSOYKRLAKSTLLILPLFGVHMVFAVFP 348
Db 294 VGSIMWNFVLFIGIIVILVQKLOSPDMGNESSIYLRLARSTLLILPLFGIHYTVFAFSP 353
QY 349 ISISSKYQILFELCLGSFQGLVAVLYCFLNSEVQCEBKRWRSRCPTPSASRDYRVCGS 408
Db 354 ENVSKEERLVFELGLGSFQGVVAVLYCFLNGEVAQAEIKRWRSWKVNRFTWDFKRRHP 413
QY 409 SFRNGSEGALQPHRGSRAQS 429
Db 414 SLASSGVNGGTQLSILSKSSS 434
```

Search completed: June 22, 2004, 09:05:00

Job time : 50 secs

The present sequence is a human G-protein coupled receptor (GPCR) used for comparison with the seven transmembrane domain of a novel GPCR designated h1571. h1571 GPCR polynucleotides and polypeptides may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GPCR expression. Such diseases includes immune, haematological, fibrotic, hepatic and respiratory disorders including asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic infections, chronic inflammatory diseases, organ-specific autoimmunity (e.g. rheumatoid arthritis), autoimmune diseases, cystic fibrosis and, in graft rejection, graft versus host disease, organ-specific autoimmunity.

CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens
CC in the production of antibodies against GPCR and in assays to identify
CC modulators (agonists and antagonists) of GPCR expression and activity.
CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
CC used as diagnostic agents for detecting the presence of GPCR polypeptides
CC in samples

XX SQ Sequence 438 AA;

Query Match 100.0%; Score 2342; DB 4; Length 438;

Best Local Similarity 100.0%; Pred. No. 1e-226;

Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPCRFHLEIQEBETKCAELLRSQTEKHKACSGWMDNIT 60
DB 1 MRTLPPALLTCWLLAPVNSIHPCRFHLEIQEBETKCAELLRSQTEKHKACSGWMDNIT 60
QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGSDPEDESKI 120
DB 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGSDPEDESKI 120
QY 121 TFYILVKAITYTLGYSVSLMSLATGSIILCLPRKHLCTRNYIHLNLFSLFIRRAISVLVKD 180
DB 121 TFYILVKAITYTLGYSVSLMSLATGSIILCLPRKHLCTRNYIHLNLFSLFIRRAISVLVKD 180
QY 181 DVLVSSSGTLHCPDPQSPSSWGCKLSLVFLQYCI MANFFWLLVEGLYHTLIVAMLPERRC 240
DB 181 DVLVSSSGTLHCPDPQSPSSWGCKLSLVFLQYCI MANFFWLLVEGLYHTLIVAMLPERRC 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGWDNDHSVPWWVIRIPILISIVNFVLI 300
DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGWDNDHSVPWWVIRIPILISIVNFVLI 300
QY 301 SIIRILLOKLTSPDVGGNDQSQYKRLAKSTLLILPLFGVHYMVFAVPISSSKYQILFE 360
DB 301 SIIRILLOKLTSPDVGGNDQSQYKRLAKSTLLILPLFGVHYMVFAVPISSSKYQILFE 360
QY 361 LCLGSFQGLVAVLYCFNLSEVQCELRKWRRCPTPSASRDYRVCSSFRNGSEGLQ 420
DB 361 LCLGSFQGLVAVLYCFNLSEVQCELRKWRRCPTPSASRDYRVCSSFRNGSEGLQ 420
QY 421 FHRGSAQSFLOTETSVI 438
DB 421 FHRGSAQSFLOTETSVI 438

RESULT 2

ABB79170

ID ABB79170 standard; protein; 438 AA.

XX AC

XX AC ABB79170;

XX DT 07-AUG-2002 (first entry)

XX DE Human VPAC2 receptor protein SEQ ID NO:10.

XX KW VPAC2 receptor; vasoactive intestinal peptide receptor; VIP; cytostatic;

XX KW vasoactive intestinal peptide; muscle mass regulator; antibacterial;

XX KW immunosuppressive; immunomodulator; antiinflammatory; infection; sepsis;

XX KW skeletal muscle atrophy; autoimmune disease; infectious disease; cancer;

XX KW cachexia; chronic inflammation; congestive heart failure; sarcopenia;

XX KW AIDS; genetic disorder; muscular dystrophy; neurodegenerative disease.

XX OS Homo sapiens.

XX PN WO200235240-A2.

XX PD 02-MAY-2002.

XX PF 22-OCT-2001; 2001WO-US043882.

XX PR 23-OCT-2000; 2000US-00694519.

XX (PROC) PROCTER & GAMBLE CO.

XX Isfort RJ, Sheldon RJ;

XX WPI; 2002-471451/50.

XX Identifying candidate compounds for regulating skeletal muscle mass or

XX function by contacting test compound with vasoactive intestinal peptide

XX receptors or cell expressing the receptor.

XX Example 1; Page 77-78; 87pp; English.

XX The present invention describes a method for identifying candidate

XX compounds (CC) for regulating skeletal muscle mass or function. The

XX method involves contacting a test compound (TC) with a vasoactive

XX intestinal peptide receptors (VPAC) or cell expressing VPAC receptor and

XX determining whether TC binds to VPAC receptor or TC that activates the

XX VPAC receptors, where the TC that binds to or activates VPAC is

XX identified as CC. The method can be used for identifying CC for

XX regulating skeletal mass or function. Other methods from the present

XX invention can be used for: identifying CC that prolong or augment the

XX activation of VPAC receptor or VPAC receptor signal transduction pathway;

XX identifying CC for increasing VPAC receptor expression; identifying CC

XX for increasing the expression of vasoactive intestinal peptide (VIP) or a

XX VIP analogue; increasing skeletal mass or function in a subject; and for

XX treating skeletal muscle atrophy in a subject. A pharmaceutical

XX composition comprising a safe and effective amount of a VPAC receptor

XX agonist can be used for modulating skeletal muscle atrophy which includes

XX broken bones, denervation/nerve damage due to surgery, bed rest,

XX autoimmune disease, infectious disease, glucocorticoid use for unrelated

XX conditions, sepsis due to infection or other causes, nutrient limitation

XX due to illness or starvation, cancer, cachexia, chronic inflammation,

XX AIDS cachexia, COPD, congestive heart failure, sarcopenia and genetic

XX disorders, e.g., muscular dystrophies, neurodegenerative diseases. The

XX present sequence represents a VPAC2 receptor which is given in the

XX exemplification of the present invention

XX SQ Sequence 438 AA;

Query Match 100.0%; Score 2342; DB 5; Length 438;

Best Local Similarity 100.0%; Pred. No. 1e-226;

Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPCRFHLEIQEBETKCAELLRSQTEKHKACSGWMDNIT 60

DB 1 MRTLPPALLTCWLLAPVNSIHPCRFHLEIQEBETKCAELLRSQTEKHKACSGWMDNIT 60

QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGSDPEDESKI 120

DB 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGSDPEDESKI 120

QY 121 TFYILVKAITYTLGYSVSLMSLATGSIILCLPRKHLCTRNYIHLNLFSLFIRRAISVLVKD 180

DB 121 TFYILVKAITYTLGYSVSLMSLATGSIILCLPRKHLCTRNYIHLNLFSLFIRRAISVLVKD 180

QY 181 DVLVSSSGTLHCPDPQSPSSWGCKLSLVFLQYCI MANFFWLLVEGLYHTLIVAMLPERRC 240

DB 181 DVLVSSSGTLHCPDPQSPSSWGCKLSLVFLQYCI MANFFWLLVEGLYHTLIVAMLPERRC 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGWDNDHSVPWWVIRIPILISIVNFVLI 300

DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGWDNDHSVPWWVIRIPILISIVNFVLI 300

QY 301 SIIRILLOKLTSPDVGGNDQSQYKRLAKSTLLILPLFGVHYMVFAVPISSSKYQILFE 360

DB 301 SIIRILLOKLTSPDVGGNDQSQYKRLAKSTLLILPLFGVHYMVFAVPISSSKYQILFE 360

QY 361 LCLGSFQGLVAVLYCFNLSEVQCELRKWRRCPTPSASRDYRVCSSFRNGSEGLQ 420

DB 361 LCLGSFQGLVAVLYCFNLSEVQCELRKWRRCPTPSASRDYRVCSSFRNGSEGLQ 420

```

QY 421 FHRGSAQSFLQTETSVI 438
DB 421 FHRGSAQSFLQTETSVI 438

RESULT 3
AAU31575
ID AAU31575 standard; protein; 439 AA.
AC AAU31575;
XX
XX 18-DEC-2001 (first entry)
XX
XX Novel human secreted protein #2066.
XX
XX Human; vaccination; gene therapy; nutritional supplement;
XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200179449-A2.
XX
XX 25-OCT-2001.
XX
XX 16-APR-2001; 2001WO-008656.
XX
XX 18-APR-2000; 2000US-00552929.
XX 26-JAN-2001; 2001US-00770160.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-611725/70.
XX
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
XX vaccination, testing and therapy.
XX
XX Claim 20; Page 461; 765pp; English.
XX
XX The invention relates to novel human secreted polypeptides. The
XX polypeptides and antibodies to the polypeptides are useful for
XX determining the presence of or predisposition to a disease associated
XX with altered levels of polypeptides. The polypeptides are also useful for
XX identifying agents (agonists and antagonists) that bind to them. Cells
XX expressing the proteins are useful for identifying a therapeutic agent
XX for use in treatment of a pathology related to aberrant expression or
XX physiological interactions of the polypeptide. Vectors comprising the
XX nucleic acids encoding the polypeptides and cells genetically engineered
XX to express them are also useful for producing the proteins. The proteins
XX are useful in genetic vaccination, testing and therapy, and can be used
XX as nutritional supplements. They may be used to increase stem cell
XX proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
XX and/or nerve tissue growth or regeneration; immune suppression and/or
XX stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
XX AAU29510-AAU3304 represent the amino acid sequences of novel human
XX secreted proteins of the invention
XX
XX Sequence 439 AA;

Query Match 100.0%; Score 2342; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 1e-226;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSHPHCRFHEIQETKCAELLRSQTEKHKACSGWQDIT 60
DB 1 MRTLPPALLTCWLLAPVNSHPHCRFHEIQETKCAELLRSQTEKHKACSGWQDIT 60

QY 61 CWRPANYGETVTVPCKVFSNFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDSKI 120
DB 61 CWRPANYGETVTVPCKVFSNFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDSKI 120

121 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFSLFSLRAISVLVKD 180
DB 121 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFSLFSLRAISVLVKD 180

QY 181 DVLYSSSGTLLHCPDQPSWVGCKLSLVFLOYCINANFFWLLVEGLYHLTLVAMLPERRC 240
DB 181 DVLYSSSGTLLHCPDQPSWVGCKLSLVFLOYCINANFFWLLVEGLYHLTLVAMLPERRC 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIVNFVLF 300
DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIVNFVLF 300

QY 301 SIIRILLQKLTSPDVGNDQSYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360
DB 301 SIIRILLQKLTSPDVGNDQSYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360

QY 361 LCLGSFQGLVAVLYCFNLSEVOCELKRWKRSRCPSPASRDYRVCGSSFSRNGSEGALQ 420
DB 361 LCLGSFQGLVAVLYCFNLSEVOCELKRWKRSRCPSPASRDYRVCGSSFSRNGSEGALQ 420

QY 421 FHRGSAQSFLQTETSVI 438
DB 421 FHRGSAQSFLQTETSVI 438

RESULT 4
AAW80308
ID AAW80308 standard; protein; 438 AA.
XX
XX AAW80308;
XX
XX 11-JAN-1999 (first entry)
XX
XX Human PACAP/VIP R-2 receptor amino acid sequence.
XX
XX Human; energy homeostasis peptide hormone receptor; PACAP/VIP R-2;
XX pituitary adenylate cyclase activating polypeptide;
XX vasoactive intestinal polypeptide;
XX cAMP-mediated signal transduction pathway.
XX
XX Homo sapiens.
XX
XX US5831051-A.
XX
XX 03-NOV-1998.
XX
XX 03-OCT-1995; 95US-00538816.
XX
XX 09-MAY-1995; 95US-00437466.
XX (UVRQ ) UNIV ROCKEFELLER.
XX
XX Wei Y, Mojsov S;
XX
XX WPI; 1998-609326/51.
XX N-PSDB; AAV66581.
XX
XX DNA encoding human energy homeostasis peptide hormone receptors - useful
XX for producing e.g. recombinant receptor proteins.
XX
XX Claim 1; Fig 1A-B; 45pp; English.
XX
XX The present sequence represents a human energy homeostasis peptide
XX hormone receptor called PACAP/VIP R-2. Pituitary adenylate cyclase
XX activating polypeptide (PACAP) and vasoactive intestinal polypeptide
XX (VIP) are structurally related proteins with multiple physiological
XX effects. The present receptor is coupled to the cAMP-mediated signal
XX transduction pathway
XX
XX Sequence 438 AA;

Query Match 99.5%; Score 2331; DB 2; Length 438;
Best Local Similarity 99.5%; Pred. No. 1.3e-225;

```


Matches 436; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGVWDNIT 60
 DB 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGVWDNIT 60

QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPDESKI 120
 DB 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPDESKI 120

QY 121 TFYILVKAITYLGYSVLSMLATGSIILCLFRKLHCTRYIHLNLFILRAISVLVKD 180
 DB 121 TFYILVKAITYLGYSVLSMLATGSIILCLFRKLHCTRYIHLNLFILRAISVLVKD 180

QY 181 DVLYSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLLVAMLP PRRC 240
 DB 181 DVLYSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLLVAMLP PRRC 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSPVWVIRIPILISIVNFVFI 300
 DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSPVWVIRIPILISIVNFVFI 300

QY 301 SIIRILLOKLTSPDVGGNDQSKYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360
 DB 301 SIIRILLOKLTSPDVGGNDQSKYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360

QY 361 LCLGSFQGLVAVLYCFLNSEVQCELCRKRWSRCPTPSASRDYRVCGSFSRNGSEGAQ 420
 DB 361 LCLGSFQGLVAVLYCFLNSEVQCELCRKRWSRCPTPSASRDYRVCGSFSRNGSEGAQ 420

QY 421 FHRGSAQSFLQTETSVI 438
 DB 421 FHRGSAQSFLQTETSVI 438

RESULT 5

AAW92972

ID AAW92972 standard; protein; 438 AA.

XX AC AAW92972;

XX 20-MAR-2003 (revised)

DT 14-MAY-1999 (first entry)

XX Human PACAP/VIP R-2 protein.

DE PACAP/VIP R-2; energy homeostasis peptide hormone receptor; VIP;

XX pituitary adenylate cyclase; PACAP; vasoactive intestinal peptide;

KW PACAP/VIP R2B; detection; modulation; diagnosis; treatment; cancer;

KW pre-cancerous lesion; viral infection; metabolic; neuroendocrine;

KW neurotransmitter; hormone; disorder; insulin secretion; antidiabetic;

KW reproductive function; anticancer; antiviral; PACAP-27; PACAP-38;

KW secretin; human.

XX OS Homo sapiens.

XX PN US5882899-A.

XX PD 16-MAR-1999.

XX PF 12-MAY-1998; 98US-00076651.

XX PR 09-MAY-1995; 95US-00437466.

XX PR 03-OCT-1995; 95US-00538816.

XX PA (UYRQ) UNIV ROCKSFELLER.

XX PI Wei Y, Mojsos S;

XX DR WPI; 1999-214065/18.

XX DR N-PSDB; AAX02878.

XX PT New second common pituitary adenylate cyclase activating

PT polypeptide/vasoactive intestinal polypeptides - useful for control of
 PT energy homeostasis, including insulin secretion.

XX Claim 1; Fig 1A-B; 45pp; English.

XX This invention describes novel energy homeostasis peptide hormone
 CC receptors representing a second common pituitary adenylate cyclase
 CC activating polypeptide/vasoactive intestinal polypeptide R-2 (PACAP/VIP R
 CC -2) and PACAP/VIP R2B. The products of the invention can be used for
 CC detection of the presence/expression of the receptors, the modulation of
 CC expression of the receptors, or the addition of the receptors or their
 CC fragments can be used to treat or diagnose cancer, pre-cancerous lesions,
 CC viral infections, or metabolic, neuroendocrine and/or neurotransmitter
 CC hormone disorders, control energy homeostasis, including insulin
 CC secretion, and modulate reproductive function. The receptors have
 CC antidiabetic, anticancer and antiviral activity and are capable of
 CC binding to PACAP-27, PACAP-38, VIP, and secretin. (Updated on 20-MAR-2003
 CC to correct PF field.)

XX Sequence 438 AA;

Query Match 99.5%; Score 2331; DB 2; Length 438;

Best Local Similarity 99.5%; Pred. No. 1.3e-225;

Matches 436; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGVWDNIT 60

DB 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGVWDNIT 60

QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPDESKI 120

DB 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPDESKI 120

QY 121 TFYILVKAITYLGYSVLSMLATGSIILCLFRKLHCTRYIHLNLFILRAISVLVKD 180

DB 121 TFYILVKAITYLGYSVLSMLATGSIILCLFRKLHCTRYIHLNLFILRAISVLVKD 180

QY 181 DVLYSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLLVAMLP PRRC 240

DB 181 DVLYSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLLVAMLP PRRC 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSPVWVIRIPILISIVNFVFI 300

DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSPVWVIRIPILISIVNFVFI 300

QY 301 SIIRILLOKLTSPDVGGNDQSKYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360

DB 301 SIIRILLOKLTSPDVGGNDQSKYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360

QY 361 LCLGSFQGLVAVLYCFLNSEVQCELCRKRWSRCPTPSASRDYRVCGSFSRNGSEGAQ 420

DB 361 LCLGSFQGLVAVLYCFLNSEVQCELCRKRWSRCPTPSASRDYRVCGSFSRNGSEGAQ 420

QY 421 FHRGSAQSFLQTETSVI 438

DB 421 FHRGSAQSFLQTETSVI 438

RESULT 6

AAW48122

ID AAW48122 standard; protein; 438 AA.

XX AC AAW48122;

XX 05-MAR-2002 (first entry)

XX Human PACAP/VIP R-2 receptor.

XX Human; PACAP/VIP R-2; receptor; antidiabetic; anti-infertility;

XX energy homeostasis; peptide hormone; Vasoactive Intestinal Polypeptide;

XX Pituitary Adenylate Cyclase Activating Polypeptide; insulin secretion;

XX reproductive function; diabetes; reproductive dysfunction; brain;

XX adipocytes; pancreas; skeletal muscle; stomach; kidney; heart.

```
XX OS Homo sapiens.
XX PN US6316596-B1.
XX PD 13-NOV-2001.
XX PF 09-DEC-1998; 98US-00208394.
XX PR 09-MAY-1995; 95US-00437466.
XX PR 03-OCT-1995; 95US-00538816.
XX PR 12-MAY-1998; 98US-00076651.
XX PA (UYRQ ) UNIV ROCKEFELLER.
XX PI Mojsos S, Wei Y;
XX PR WPI; 2002-096549/13.
XX DR N-PSDB; ABA95313.
XX PT New recombinant human energy homeostasis peptide hormone receptor
XX PT PACAP/VIP R-2, e.g. useful for treating diabetes or reproductive
XX PT dysfunction.
XX PS Claim 1; Fig 1; 45pp; English.
XX CC The present sequence is the protein sequence for an human energy
XX CC homeostasis peptide hormone receptor (PACAP/VIP R-2). PACAP is Pituitary
XX CC Adenylate Cyclase Activating Polypeptide, and VIP is Vasoactive
XX CC Intestinal Polypeptide. PACAP/VIP R-2 binds to both PACAP and VIP and is
XX CC distributed in tissues including the brain, adipocytes, pancreas,
XX CC skeletal muscle, stomach, kidney and heart. PACAP/VIP R-2 is useful as a
XX CC receptor for a metabolic, neuroendocrine and/or neurotransmitter peptide
XX CC hormone, to control energy homeostasis, including stimulating insulin
XX CC secretion, and as a modulator of reproductive function. PACAP/VIP R-2 is
XX CC also potentially useful in therapeutic, diagnostic and drug screening
XX CC applications, e.g. for treating diabetes and reproductive dysfunction
XX CC
XX SQ Sequence 438 AA;

Query Match 99.5%; Score 2331; DB 5; Length 438;
Best Local Similarity 99.5%; Pred. No. 1.3e-225;
Matches 436; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRTLPPALATCWLAPVNSIHPCRFHLETOEETKCAELLRSQTEKHKACSGVNDIT 60
DB 1 MRTLPPALATCWLAPVNSIHPCRFHLETOEETKCAELLRSQTEKHKACSGVNDIT 60
QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNTSDGMSSETFPDFVDACGYSDPEDESKI 120
DB 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNTSDGMSSETFPDFVDACGYSDPEDESKI 120
QY 121 TFYLIVKAIYTLGYSVLSMLATGSIILCPRLKHTCRNYIHLNLFSLIRALISVLVKD 180
DB 121 TFYLIVKAIYTLGYSVLSMLATGSIILCPRLKHTCRNYIHLNLFSLIRALISVLVKD 180
QY 181 DVLVSSSGTLHCPDQPSWGWCKLSLVFLQVCIMANFFWLLVEGLYHLTLVAMPVPRRC 240
DB 181 DVLVSSSGTLHCPDQPSWGWCKLSLVFLQVCIMANFFWLLVEGLYHLTLVAMPVPRRC 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGWDNDHSPVWVIRIPILISIIYVNFVFI 300
DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGWDNDHSPVWVIRIPILISIIYVNFVFI 300
QY 301 SIIRILQKLTSPDVGNDQGYRLAKSTLLPLFGVHWVWFAVPFISISKYQLIFE 360
DB 301 SIIRILQKLTSPDVGNDQGYRLAKSTLLPLFGVHWVWFAVPFISISKYQLIFE 360
QY 361 LCLGSFQGLVAVLYCFINSVQCEKELKRSRCPTPSASRDYRVCGSSFRNGSEGLAQ 420
DB 361 LCLGSFQGLVAVLYCFINSVQCEKELKRSRCPTPSASRDYRVCGSSFRNGSEGLAQ 420
QY 421 FHGRSRAQSFLQTETSVI 438
```

```
DB 421 FHGRSRAQSFLQTETSVI 438
RESULT 7
ID ABB79172
XX ABB79172 standard; protein; 438 AA.
XX AC ABB79172;
XX 07-AUG-2002 (first entry)
XX DE Human VPAC2 receptor protein SEQ ID NO:12.
XX KW VPAC receptor; vasoactive intestinal peptide receptor; VIP; cytostatic;
XX KW vasoactive intestinal peptide; muscle mass regulation; antibacterial;
XX KW immunosuppressive; immunomodulator; antiinflammatory; infection; sepsis;
XX KW skeletal muscle atrophy; autoimmune disease; infectious disease; cancer;
XX KW cachexia; chronic inflammation; congestive heart failure; sarcopenia;
XX KW AIDS; genetic disorder; muscular dystrophy; neurodegenerative disease.
XX OS Homo sapiens.
XX PN WO200235240-A2.
XX PD 02-MAY-2002.
XX PF 22-OCT-2001; 2001WO-US043882.
XX PR 23-OCT-2000; 2000US-00694519.
XX PA (PROC ) PROCTER & GAMBLE CO.
XX PI Isfort RJ, Sheldon RJ;
XX DR WPI; 2002-471451/50.
XX PT Identifying candidate compounds for regulating skeletal muscle mass or
XX PT function by contacting test compound with vasoactive intestinal peptide
XX PT receptors or cell expressing the receptor.
XX PS Disclosure; Page 80-81; 87pp; English.
XX CC The present invention describes a method for identifying candidate
XX CC compounds (CC) for regulating skeletal muscle mass or function. The
XX CC method involves contacting a test compound (TC) with a vasoactive
XX CC intestinal peptide receptors (VPAC) or cell expressing VPAC receptor and
XX CC determining whether TC binds to VPAC receptor or TC that activates the
XX CC VPAC receptors, where the TC that binds to or activates VPAC is
XX CC identified as CC. The method can be used for identifying CC for
XX CC regulating skeletal mass or function. Other methods from the present
XX CC invention can be used for: identifying CC that prolong or augment the
XX CC activation of VPAC receptor or VPAC receptor signal transduction pathway;
XX CC identifying CC for increasing VPAC receptor expression; identifying CC
XX CC for increasing the expression of vasoactive intestinal peptide (VIP) or a
XX CC VIP analogue; increasing skeletal mass or function in a subject; and for
XX CC treating skeletal muscle atrophy in a subject. A pharmaceutical
XX CC composition comprising a safe and effective amount of a VPAC receptor
XX CC agonist can be used for modulating skeletal muscle atrophy which includes
XX CC skeletal muscle atrophy induced by disuse due to surgery, bed rest,
XX CC broken bones, denervation/nerve damage due to spinal cord injury,
XX CC autoimmune disease, infectious disease, glucocorticoid use for unrelated
XX CC conditions, sepsis due to infection or other causes, nutrient limitation
XX CC due to illness or starvation, cancer, cachexia, chronic inflammation,
XX CC AIDS cachexia, COPD, congestive heart failure, sarcopenia and genetic
XX CC disorders, e.g., muscular dystrophies, neurodegenerative diseases. The
XX CC present sequence represents a VPAC2 receptor which is given in the
XX CC exemplification of the present invention
XX SQ Sequence 438 AA;
```

Query Match 99.5%; Score 2331; DB 5; Length 438;
Best Local Similarity 99.5%; Pred. No. 1.3e-225;

```

Matches 436; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHLEIQEETKCAELLSQTEKHKACSGVMDNIT 60
DB 1 MRTLPPALLTCWLLAPVNSIHPECRFHLEIQEETKCAELLSQTEKHKACSGVMDNIT 60
QY 61 CWRPANVGSETVTPCPKVSNEFYSKAGNISKNCTSDGWSSETPDPFDVACGYSDPDESKI 120
DB 61 CWRPANVGSETVTPCPKVSNEFYSKAGNISKNCTSDGWSSETPDPFDVACGYSDPDESKI 120
QY 121 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRYNIHLNLFSLRAISVLVD 180
DB 121 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRYNIHLNLFSLRAISVLVD 180
QY 181 DVLYSSTGLHCPDQPSWVGCKLSLVFLQYICIMANFFWLLVEGLYHLTLLVAMLPPRR 240
DB 181 DVLYSSTGLHCPDQPSWVGCKLSLVFLQYICIMANFFWLLVEGLYHLTLLVAMLPPRR 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGWDNDHSPVWVIRIPILISIIIVNVLFI 300
DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGWDNDHSPVWVIRIPILISIIIVNVLFI 300
QY 301 SIIRILLOKLTSPDVGGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQILFE 360
DB 301 SIIRILLOKLTSPDVGGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQILFE 360
QY 361 LCLGSFQGLVAVLYCFLNSEVQCELRKWRRCPTPSASRDYRVCGSSFSRNGSEGAQ 420
DB 361 LCLGSFQGLVAVLYCFLNSEVQCELRKWRRCPTPSASRDYRVCGSSFSRNGSEGAQ 420
QY 421 FHRGSRQAQSFLOTETSVI 438
DB 421 FHRGSRQAQSFLOTETSVI 438

```

RESULT 8

* ABG27816

ID ABG27816 standard; protein; 454 AA.

XX AC ABG27816;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #27807.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX OS food supplement; medical imaging; diagnostic; genetic disorder.

XX PN Homo sapiens.

XX PD WO200175067-A2.

XX PF 11-OCT-2001.

XX PR 30-MAR-2001; 2001MO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX PR WPI; 2001-639362/73.

XX DR N-PSDB; AAS92003.

XX PT New isolated polynucleotide and encoded polypeptides, useful in

XX PT diagnostics, forensics, gene mapping, identification of mutations

XX PT responsible for genetic disorders or other traits and to assess

XX PT biodiversity.

XX PS Claim 20; SEQ ID NO 58175; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 454 AA;

Query Match 99.5%; Score 2331; DB 4; Length 454;

Best Local Similarity 99.5%; Pred. No. 1.4e-225;

Matches 436; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHLEIQEETKCAELLSQTEKHKACSGVMDNIT 60

DB 17 MRTLPPALLTCWLLAPVNSIHPECRFHLEIQEETKCAELLSQTEKHKACSGVMDNIT 76

QY 61 CWRPANVGSETVTPCPKVSNEFYSKAGNISKNCTSDGWSSETPDPFDVACGYSDPDESKI 120

DB 77 CWRPANVGSETVTPCPKVSNEFYSKAGNISKNCTSDGWSSETPDPFDVACGYSDPDESKI 136

QY 121 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRYNIHLNLFSLRAISVLVD 180

DB 137 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRYNIHLNLFSLRAISVLVD 196

QY 181 DVLYSSTGLHCPDQPSWVGCKLSLVFLQYICIMANFFWLLVEGLYHLTLLVAMLPPRR 240

DB 197 DVLYSSTGLHCPDQPSWVGCKLSLVFLQYICIMANFFWLLVEGLYHLTLLVAMLPPRR 256

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGWDNDHSPVWVIRIPILISIIIVNVLFI 300

DB 257 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGWDNDHSPVWVIRIPILISIIIVNVLFI 316

QY 301 SIIRILLOKLTSPDVGGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQILFE 360

DB 317 SIIRILLOKLTSPDVGGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQILFE 376

QY 361 LCLGSFQGLVAVLYCFLNSEVQCELRKWRRCPTPSASRDYRVCGSSFSRNGSEGAQ 420

DB 377 LCLGSFQGLVAVLYCFLNSEVQCELRKWRRCPTPSASRDYRVCGSSFSRNGSEGAQ 436

QY 421 FHRGSRQAQSFLOTETSVI 438

DB 437 FHRGSRQAQSFLOTETSVI 454

RESULT 9

AAE07961

ID AAE07961 standard; protein; 438 AA.

XX AC AAE07961;

XX DT 01-NOV-2001 (first entry)

XX DE Human vasoactive intestinal peptide (VIP) receptor subtype, VPAC2.

XX KW Human; female sexual dysfunction; FSD; female sexual arousal dysfunction;

XX KW FSAD; neutral endopeptidase inhibitor; I.NEP; enkephalinase;

KW gynaecological; vasoactive intestinal peptide receptor subtype; VIP;
 KW VPAC2; endopeptidase-2.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= Signal_peptide
 FT Protein 24..438
 FT /label= Human_mature_VPAC2
 XX EPI097719-A1.
 PN 09-MAY-2001.
 XX 03-NOV-2000; 2000EP-00309722.
 XX 08-NOV-1999; 99GB-00026437.
 PR 18-FEB-2000; 2000GB-00004021.
 PR 26-MAY-2000; 2000GB-00013001.
 PR 05-JUL-2000; 2000GB-00016563.
 PR 12-JUL-2000; 2000GB-00017141.
 XX (PFIZ) PFIZER LTD.
 PA (PFIZ) PFIZER INC.
 XX Maw GN, Wayman CP;
 PI
 XX WPI; 2001-309880/33.
 DR N-PSDB; AAD14533.
 XX
 -PT Treating females suffering from female sexual dysfunction, preferably
 -PT female sexual arousal dysfunction using a neutral endopeptidase inhibitor
 -PT that potentiates CAMP in female genitalia.
 XX
 PS Disclosure; Page 105; 124pp; English.
 XX
 -CC The present invention relates to a method for treating female sexual
 -CC dysfunction (FSD), preferably female sexual arousal dysfunction (FSAD).
 -CC The method comprising using an agent, an inhibitor of neutral
 -CC endopeptidase (NEP) EC 3.4.24.11 or I:NEP, which is capable of
 -CC potentiating CAMP (which enhances female genital blood flow) in the
 -CC sexual genitalia of the females. NEP is also known as enkephalinase or
 -CC endopeptidase-2. The agent is optionally admixed with a diluent, carrier
 -CC or excipient. The method restores a normal sexual arousal response,
 -CC particularly increased blood flow leading to vaginal, clitoral and labial
 -CC engorgement. This will result in increased vaginal lubrication via plasma
 -CC transduction, increased vaginal compliance and increased genital (e.g.
 -CC vaginal and clitoral) sensitivity. The present sequence is human
 -CC vasoactive intestinal peptide (VIP) receptor subtype, VPAC2 used in the
 -CC method of the invention
 XX
 SQ Sequence 438 AA;
 Query Match 99.4%; Score 2327; DB 4; Length 438;
 Best Local Similarity 99.3%; Pred. No. 3.3e-225;
 Matches 435; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MRTLPPALLTCWLLAPVNSHPECRFHLQTEERTKCAELLRSQTEKHKACSGWMDNIT 60
 DB 1 MRTLPPALLTCWLLAPVNSHPECRFHLQTEERTKCAELLRSQTEKHKACSGWMDNIT 60
 QY 61 CWRPANVGETVTPCPKVFNSFMSLATGSIILCLFRKLHCTRNHYHLNLFILRAISVLVKD 120
 DB 61 CWRPANVGETVTPCPKVFNSFMSLATGSIILCLFRKLHCTRNHYHLNLFILRAISVLVKD 120
 QY 121 TFYILVKAITYLGVSVLSMSLATGSIILCLFRKLHCTRNHYHLNLFILRAISVLVKD 180
 DB 121 TFYILVKAITYLGVSVLSMSLATGSIILCLFRKLHCTRNHYHLNLFILRAISVLVKD 180
 QY 181 DVLVSSSGTLHCPDQPSFMSVCKSLVFLQYCI MANFFWLLVEGYLHTLLVAMLP PPRC 240
 DB 181 DVLVSSSGTLHCPDQPSFMSVCKSLVFLQYCI MANFFWLLVEGYLHTLLVAMLP PPRC 240

QY 241 FLAYLLICWGLPTVCIGAWTAARLYLEDTCGWDTNDHSVPWWVIRIPILISIVNVLFI 300
 DB 241 FLAYLLICWGLPTVCIGAWTAARLYLEDTCGWDTNDHSVPWWVIRIPILISIVNVLFI 300
 QY 301 SIIRILLOKLTSPDVGGNDQSYKRLAKSTLLILLPLFGVHYMVFAVFFPISISSKYQIILFE 360
 DB 301 SIIRILLOKLTSPDVGGNDQSYKRLAKSTLLILLPLFGVHYMVFAVFFPISISSKYQIILFE 360
 QY 361 LCLGSFQGLVAVLYCFNLSEVQCELCMKWRSCPTPSASRDYRVCGSFSGRNGSEGALQ 420
 DB 361 LCLGSFQGLVAVLYCFNLSEVQCELCMKWRSCPTPSASRDYRVCGSFSGRNGSEGALQ 420
 QY 421 FHRGSRQSFLOTETSVI 438
 DB 421 FHRASRAQSFLQTETSVI 438

RESULT 10
 AAE07925
 ID AAE07925 standard; protein; 438 AA.
 XX AAE07925;
 AC AAE07925;
 DT 01-NOV-2001 (first entry)
 XX Human vasoactive intestinal peptide (VIP) receptor protein, VPAC2.
 DE Human; female sexual dysfunction; FSD; female sexual arousal dysfunction;
 XX FSAD; neuropeptide Y; NPY; gynaecological; vasoactive intestinal peptide;
 KW VIP receptor; VPAC2; pituitary adenylate cyclase-activating peptide;
 KW PACAP; VIP2; helodermin-preferring VIP receptor.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Peptide 1..23
 FT Protein /label= Signal_peptide
 FT 24..438
 XX /label= Human_mature_VPAC2_protein
 PN EPI097718-A1.
 XX 09-MAY-2001.
 XX 03-NOV-2000; 2000EP-00309720.
 PR 08-NOV-1999; 99GB-00026437.
 PR 18-FEB-2000; 2000GB-00004021.
 PR 26-MAY-2000; 2000GB-00013001.
 PR 05-JUL-2000; 2000GB-00016563.
 PR 12-JUL-2000; 2000GB-00017141.
 XX (PFIZ) PFIZER LTD.
 PA (PFIZ) PFIZER INC.
 XX Maw GN, Wayman CP;
 PI
 XX WPI; 2001-319199/34.
 DR N-PSDB; AAD14523.
 XX
 -PT Treating females suffering from female sexual dysfunction, preferably
 -PT female sexual arousal dysfunction using a neuropeptide Y inhibitor that
 -PT potentiates CAMP in female genitalia.
 XX
 PS Disclosure; Page 143-145; 165pp; English.
 XX
 -CC The patent discloses a method for the treatment of a female suffering
 -CC from female sexual dysfunction (FSD), preferably female sexual arousal
 -CC dysfunction (FSAD) by the use of an agent which is an inhibitor of
 -CC neuropeptide Y (NPY). The agent is capable of potentiating CAMP which
 -CC enhances female genital (e.g. vaginal or clitoral) blood flow in the
 -CC sexual genitalia of the female and is optionally admixed with a diluent

CC	carrier or excipient. The method restores a normal sexual arousal	XX	08-NOV-1999; 99GB-00026437.
CC	response namely, increased blood flow leading to vaginal, clitoral and	PR	18-FEB-2000; 2000GB-00004021.
CC	labial engorgement. This will result in increased vaginal lubrication via	PR	26-MAY-2000; 2000GB-00013001.
CC	plasma transduction, increased vaginal compliance and increased genital	PR	05-JUL-2000; 2000GB-00016563.
CC	(e.g. vaginal and clitoral) sensitivity. The method is used for treating	PR	12-JUL-2000; 2000GB-00017141.
CC	a female suffering from FSD preferably FSAD. The present sequence is	XX	(PFIZ) PFIZER LTD.
CC	vasoactive intestinal peptide (VIP) receptor subtype, VPAC2 from human.	PA	(PFIZ) PFIZER INC.
CC	VPAC2 is also known as VIP2 or PACAP (pituitary adenylate cyclase-	XX	
CC	activating peptide). Human VIP2 was previously known as helodermin-	PI	Maw GN, Wayman CP;
CC	preferring VIP receptor. VIP is released during pelvic nerve stimulation	DR	WPI: 2001-383217/41.
CC	or sexual arousal and induces clitoral vasorelaxation via the CAMP	DR	N-PSDB; AAF84032.
XX	pathway	XX	
SQ	Sequence 438 AA;	XX	
Query Match	99.4%; Score 2327; DB 4; Length 438;	PT	Novel pharmaceutical composition for treating female sexual dysfunction,
Best Local Similarity	99.3%; Pred. No. 3.3e-225;	PT	preferably female sexual arousal disorder, comprising an agent capable of
Matches 435; Conservative	0; Mismatches 3; Indels 0; Gaps 0;	PT	potentiating CAMP in the sexual genitalia of the female.
PS	Disclosure; Page 112-113; 135pp; English.	XX	
CC	The invention provides a pharmaceutical composition for treating female	CC	sexual dysfunction (FSD), preferably female sexual arousal disorder
CC	(FSAD), or enhancing female genital (e.g. vaginal or clitoral) blood flow	CC	in a female. The composition comprises an agent capable of potentiating
CC	CAMP in the sexual genitalia of the female. The agent is an inhibitor	CC	CAMP in the sexual genitalia of the female. The agent is an inhibitor
CC	(I:PDE) of phosphodiesterase (PDE), which hydrolyzes CAMP (optionally	CC	CAMP). The agent is useful in the manufacture of a medicament for the
CC	treatment of FSD, preferably FSAD, by potentiating CAMP in the sexual	CC	genitalia. It is also useful in the manufacture of a medicament for the
CC	enhancing female genital (e.g., vaginal or clitoral) blood flow. The	CC	present sequence represents a human helodermin-preferring VIP (vasoactive
CC	intestinal peptide) receptor (VIP2/PACAP)	CC	
XX		XX	
SQ	Sequence 438 AA;	SQ	
Query Match	99.4%; Score 2327; DB 4; Length 438;	Query Match	99.4%; Score 2327; DB 4; Length 438;
Best Local Similarity	99.3%; Pred. No. 3.3e-225;	Best Local Similarity	99.3%; Pred. No. 3.3e-225;
Matches 435; Conservative	0; Mismatches 3; Indels 0; Gaps 0;	Matches 435; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
QY	1 MRTLPPALLTCWLLAPVNSIHPECFRHLIEQBEETKCAELRSQTEKHKACSGVNDNIT 60	QY	1 MRTLPPALLTCWLLAPVNSIHPECFRHLIEQBEETKCAELRSQTEKHKACSGVNDNIT 60
DB	1 MRTLPPALLTCWLLAPVNSIHPECFRHLIEQBEETKCTELLRSQTEKHKACSGVNDNIT 60	DB	1 MRTLPPALLTCWLLAPVNSIHPECFRHLIEQBEETKCTELLRSQTEKHKACSGVNDNIT 60
QY	61 CWRPANVGETVTVPCPKVFSNFYSKAGNISKNCTSDGWSSETFFDFVDACGYSPPEDSKI 120	QY	61 CWRPANVGETVTVPCPKVFSNFYSKAGNISKNCTSDGWSSETFFDFVDACGYSPPEDSKI 120
DB	61 CWRPANVGETVTVPCPKVFSNFYSKAGNISKNCTSDGWSSETFFDFVDACGYSPPEDSKI 120	DB	61 CWRPANVGETVTVPCPKVFSNFYSKAGNISKNCTSDGWSSETFFDFVDACGYSPPEDSKI 120
QY	121 TFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRNVIHNLFLSFILRAISVLVKD 180	QY	121 TFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRNVIHNLFLSFILRAISVLVKD 180
DB	121 TFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRNVIHNLFLSFILRAISVLVKD 180	DB	121 TFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRNVIHNLFLSFILRAISVLVKD 180
QY	181 DVLYSSGTLHCPDQPSWVGCKLSLVFLQYCIIMANFFWLLVEGLYHLTLVAMLPERRC 240	QY	181 DVLYSSGTLHCPDQPSWVGCKLSLVFLQYCIIMANFFWLLVEGLYHLTLVAMLPERRC 240
DB	181 DVLYSSGTLHCPDQPSWVGCKLSLVFLQYCIIMANFFWLLVEGLYHLTLVAMLPERRC 240	DB	181 DVLYSSGTLHCPDQPSWVGCKLSLVFLQYCIIMANFFWLLVEGLYHLTLVAMLPERRC 240
QY	241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPWVIRIPILISIVNVLFI 300	QY	241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPWVIRIPILISIVNVLFI 300
DB	241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPWVIRIPILISIVNVLFI 300	DB	241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPWVIRIPILISIVNVLFI 300
QY	301 SIIRILLQKLTSPDVGNDSQYKRLAKSTLILLPLFGVHYMVFAVFPPISSIKYQILFE 360	QY	301 SIIRILLQKLTSPDVGNDSQYKRLAKSTLILLPLFGVHYMVFAVFPPISSIKYQILFE 360
DB	301 SIIRILLQKLTSPDVGNDSQYKRLAKSTLILLPLFGVHYMVFAVFPPISSIKYQILFE 360	DB	301 SIIRILLQKLTSPDVGNDSQYKRLAKSTLILLPLFGVHYMVFAVFPPISSIKYQILFE 360
QY	361 LCLGSFQGLVAVLYCFNLSEVOCELKRWRSRCPFPSASRDYRVCGSSFSRNGSEGALQ 420	QY	361 LCLGSFQGLVAVLYCFNLSEVOCELKRWRSRCPFPSASRDYRVCGSSFSRNGSEGALQ 420
DB	361 LCLGSFQGLVAVLYCFNLSEVOCELKRWRSRCPFPSASRDYRVCGSSFSRNGSEGALQ 420	DB	361 LCLGSFQGLVAVLYCFNLSEVOCELKRWRSRCPFPSASRDYRVCGSSFSRNGSEGALQ 420
QY	421 FHRGSAQSFLQTETSVI 438	QY	421 FHRGSAQSFLQTETSVI 438
DB	421 FHRASRAQSFLQTETSVI 438	DB	421 FHRASRAQSFLQTETSVI 438
RESULT 11		RESULT 11	
ID	AAB85124	ID	AAB85124
AC	AAB85124 standard; protein; 438 AA.	AC	AAB85124 standard; protein; 438 AA.
XX		XX	
AC	AAB85124;	AC	AAB85124;
XX		XX	
DT	22-AUG-2001 (first entry)	DT	22-AUG-2001 (first entry)
XX		XX	
DE	Human helodermin-preferring VIP receptor (VIP2/PACAP).	DE	Human helodermin-preferring VIP receptor (VIP2/PACAP).
XX		XX	
KW	Female sexual dysfunction; FSD; female sexual arousal disorder; FSAD;	KW	Female sexual dysfunction; FSD; female sexual arousal disorder; FSAD;
KW	genital; vaginal; clitoral; blood flow; CAMP; phosphodiesterase; PDE;	KW	genital; vaginal; clitoral; blood flow; CAMP; phosphodiesterase; PDE;
KW	CMP; medicament; human; vasoactive intestinal peptide; VIP; VIP2; PACAP.	KW	CMP; medicament; human; vasoactive intestinal peptide; VIP; VIP2; PACAP.
XX		XX	
OS	Homo sapiens.	OS	Homo sapiens.
XX		XX	
PN	EP1097707-A1.	PN	EP1097707-A1.
XX		XX	
PD	09-MAY-2001.	PD	09-MAY-2001.
XX		XX	
PF	03-NOV-2000; 2000EP-00309719.	PF	03-NOV-2000; 2000EP-00309719.

CC treating skeletal muscle atrophy in a subject. A pharmaceutical
CC composition comprising a safe and effective amount of a VPAC receptor
CC agonist can be used for modulating skeletal muscle atrophy which includes
CC skeletal muscle atrophy induced by disuse due to surgery, bed rest,
CC broken bones, denervation/nerve damage due to spinal cord injury,
CC autoimmune disease, infectious disease, glucocorticoid use for unrelated
CC conditions, sepsis due to infection or other causes, nutrient limitation
CC due to illness or starvation, cancer, cachexia, chronic inflammation,
CC AIDS cachexia, COPD, congestive heart failure, sarcopenia and genetic
CC disorders, e.g., muscular dystrophies, neurodegenerative diseases. The
CC present sequence represents a VPAC2 receptor which is given in the
CC exemplification of the present invention

XX SQ Sequence 438 AA;

Query Match 99.4%; Score 2327; DB 5; Length 438;
Best Local Similarity 99.3%; Pred. No. 3.3e-225;
Matches 435; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCMLLAPVNSIHPCRFHLEIOBEETKCAELLRSQTEKHKACSGVNDIT 60
DB 1 MRTLPPALLTCMLLAPVNSIHPCRFHLEIOBEETKCAELLRSQTEKHKACSGVNDIT 60
QY 61 CWRPANGETVTVPCKVFSNFYSKAGNISKNCTSDGMSFTFPDVFVACGYSDPEDESKI 120
DB 61 CWRPANGETVTVPCKVFSNFYSKAGNISKNCTSDGMSFTFPDVFVACGYSDPEDESKI 120
QY 121 TFYLKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180
DB 121 TFYLKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180
QY 181 DVLYSSGTLHCPDPQSSWVGCKLSVFLQYCIANFFVLLVEGLYHLTLVAMLPERRC 240
DB 181 DVLYSSGTLHCPDPQSSWVGCKLSVFLQYCIANFFVLLVEGLYHLTLVAMLPERRC 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIVNVLFI 300
DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIVNVLFI 300
QY 301 SIIRILQKLTSPDVGGNDQSYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQILFE 360
DB 301 SIIRILQKLTSPDVGGNDQSYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQILFE 360
QY 361 LCLGSFQGLVVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGAQ 420
DB 361 LCLGSFQGLVVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGAQ 420
QY 421 FHRASRAQSFLOTETSVI 438
DB 421 FHRASRAQSFLOTETSVI 438

RESULT 14

ADA83955 standard; protein; 438 AA.

XX AC ADA83955;
XX AC
XX 20-NOV-2003 (first entry)
XX DE Human POM61 protein.
XX human; marker; expressed sequence tag; EST; arabidopsis; tumour;
KW stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
KW vaccine.
XX OS Homo sapiens.
XX FN WO2002103028-A2.
XX PD 27-DEC-2002.
XX FF 30-MAY-2002; 2002WO-IB004189.

XX 30-MAY-2001; 2001US-0293999P.
PR 22-OCT-2001; 2001US-0330457P.
PR 19-FEB-2002; 2002US-0357144P.
XX PA (BIOM-) BIOMEDICAL CENT.
XX PI Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;
XX WPI; 2003-175241/17.
DR N-PSDB; ADA83954.
XX PT Determining if a nucleic acid is a marker for a phenotype/cell type of
PT interest, by global comparison of expressed sequence tags known to be
PT expressed in the phenotype/cell type with all ESTs expressed in normal
PT tissue.
XX Claim 29; Page 331-333; 516pp; English.

XX The invention relates to a novel method for determining if a nucleic acid
CC is a marker for a predetermined phenotype/cell type of interest from a
CC biological species. The method comprises performing a global comparison
CC of a group of expressed sequence tags (ESTs) known to be expressed in the
CC phenotype/cell type of interest with all ESTs expressed in normal tissue
CC in order to identify ESTs that are preferentially expressed in the
CC phenotype/cell of interest. A method of the invention is useful for
CC determining whether a nucleic acid is a marker for a predetermined
CC phenotype or cell type of interest from a biological species, preferably
CC Arabidopsis or human. The cell type of interest is an abnormal cell such
CC as a tumour cell, and the predetermined phenotype is a stress-induced
CC phenotype such as hyperosmotic stress or high salt conditions. A method
CC of the invention is also useful for determining the progression of colon
CC cancer in a human, for detecting a tumour cell, and for regulating or
CC preventing the growth of a tumour cell. An antibody of the invention is
CC useful for detecting the absence or presence of peptides encoded by
CC tumour-associated markers. A polypeptide of the invention is useful as an
CC immunogen for vaccinating an animal. The present sequence represents a
CC tumour-associated antigen of the invention.

XX SQ Sequence 438 AA;

Query Match 99.4%; Score 2327; DB 6; Length 438;
Best Local Similarity 99.3%; Pred. No. 3.3e-225;
Matches 435; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCMLLAPVNSIHPCRFHLEIOBEETKCAELLRSQTEKHKACSGVNDIT 60
DB 1 MRTLPPALLTCMLLAPVNSIHPCRFHLEIOBEETKCAELLRSQTEKHKACSGVNDIT 60
QY 61 CWRPANGETVTVPCKVFSNFYSKAGNISKNCTSDGMSFTFPDVFVACGYSDPEDESKI 120
DB 61 CWRPANGETVTVPCKVFSNFYSKAGNISKNCTSDGMSFTFPDVFVACGYSDPEDESKI 120
QY 121 TFYLKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180
DB 121 TFYLKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180
QY 181 DVLYSSGTLHCPDPQSSWVGCKLSVFLQYCIANFFVLLVEGLYHLTLVAMLPERRC 240
DB 181 DVLYSSGTLHCPDPQSSWVGCKLSVFLQYCIANFFVLLVEGLYHLTLVAMLPERRC 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIVNVLFI 300
DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIVNVLFI 300
QY 301 SIIRILQKLTSPDVGGNDQSYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQILFE 360
DB 301 SIIRILQKLTSPDVGGNDQSYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQILFE 360
QY 361 LCLGSFQGLVVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGAQ 420
DB 361 LCLGSFQGLVVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGAQ 420

QY 421 FHRGSAQSFLOTETSVI 438
 DB 421 FHRGSAQSFLOTETSVI 438

RESULT 15

ABP81992
 ID ABP81992 standard; protein; 438 AA.

XX
 AC ABP81992;

XX
 DT 04-MAR-2003 (first entry)

XX
 DE Human vasoactive intestinal polypeptide receptor 2 protein SEQ ID NO:471.

XX
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.

XX
 OS Homo sapiens.

XX
 PN WO200261087-A2.

XX
 PD 08-AUG-2002.

XX
 PF 19-DEC-2001; 2001WO-US050107.

XX
 PR 19-DEC-2000; 2000US-0257144P.

XX
 *PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX
 PI Burmer GC, Roush CL, Brown JP;

XX
 DR WPI; 2003-046718/04.

XX
 DR N-PSDB; AB242841.

XX
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.

XX
 PS Disclosure; Fig 1; 523pp; English.

XX
 CC The present invention describes antigenic peptides (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be

CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention

XX
 SQ Sequence 438 AA;

Query Match 99.4%; Score 2327; DB 6; Length 438;
 Best Local Similarity 99.3%; Pred. No. 3.3e-225;
 Matches 435; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 METLLPALLTCWLLAPVNSIHPECKFHLIEIQEETKCAELLSQTEKHKACSGVWDNIT 60
 DB 1 METLLPALLTCWLLAPVNSIHPECKFHLIEIQEETKCTELLRSQTEKHKACSGVWDNIT 60
 QY 61 CWRPANVGETVTPCKVPFSNFYKAGNISKNCTSDGWSSETPPDFVDAGYDDEDESKI 120
 DB 61 CWRPANVGETVTPCKVPFSNFYKAGNISKNCTSDGWSSETPPDFVDAGYDDEDESKI 120
 QY 121 TFYILVKAIYTLGYSVLSMLATGSIILCPFKLHCTRYIHNLFLSFILRAISVLVKD 180
 DB 121 TFYILVKAIYTLGYSVLSMLATGSIILCPFKLHCTRYIHNLFLSFILRAISVLVKD 180
 QY 181 DVLYSSSGTLHCPDQPSNVGCKLSLVFLQYICIMANFFWLLVEGLYLTLLVAMLPFRR 240
 DB 181 DVLYSSSGTLHCPDQPSNVGCKLSLVFLQYICIMANFFWLLVEGLYLTLLVAMLPFRR 240
 QY 241 FLAYLLIGWGLPTVCIGAWTAARLYEDTGCDWTDNDHSVPMWVIRIPILISIIIVNVLFI 300
 DB 241 FLAYLLIGWGLPTVCIGAWTAARLYEDTGCDWTDNDHSVPMWVIRIPILISIIIVNVLFI 300
 QY 301 STIIRILLOKLTSPDVGGNDQSOYKELAKSTLLLIPLFGVHYMVFAVEPTISISSKYQILFE 360
 DB 301 STIIRILLOKLTSPDVGGNDQSOYKELAKSTLLLIPLFGVHYMVFAVEPTISISSKYQILFE 360
 QY 361 LCLGSFQGLVAVLYCFLNSEVQCELBKRWKRSRCPTPSASRDYRVCGSSFSHNGSEGAQ 420
 DB 361 LCLGSFQGLVAVLYCFLNSEVQCELBKRWKRSRCPTPSASRDYRVCGSSFSHNGSEGAQ 420
 QY 421 FHRGSAQSFLOTETSVI 438
 DB 421 FHRGSAQSFLOTETSVI 438

Search completed: June 22, 2004, 08:57:33

Job time : 63 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 22, 2004, 08:56:24 ; Search time 23 Seconds
(without alignments)
983.138 Million cell updates/sec

Title: US-09-983-000A-20
Perfect score: 2342
Sequence: 1 MRLTLPALITCWLAPVNS.....LQHRGSRAGSFLQTETSVI 438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
Result No.	Score	Query Match	Length	DB	ID	Description			
1	2331	99.5	438	2	US-08-538-816A-1	Sequence 1, Appli			
2	2331	99.5	438	2	US-09-076-651-1	Sequence 1, Appli			
3	2331	99.5	438	4	US-09-208-394-1	Sequence 1, Appli			
4	2239.5	95.6	431	2	US-08-538-816A-9	Sequence 9, Appli			
5	2239.5	95.6	431	2	US-09-076-651-9	Sequence 9, Appli			
6	2239.5	95.6	431	4	US-09-208-394-9	Sequence 9, Appli			
7	2030	86.7	437	2	US-08-538-816A-2	Sequence 2, Appli			
8	2030	86.7	437	2	US-09-076-651-2	Sequence 2, Appli			
9	2030	86.7	437	4	US-09-208-394-2	Sequence 2, Appli			
10	1153.5	49.3	467	2	US-08-811-897A-19	Sequence 19, Appl			
11	1153.5	49.3	467	2	US-08-855-213-19	Sequence 19, Appl			
12	1153.5	49.3	467	4	US-09-201-474-19	Sequence 19, Appl			
13	1151.5	49.2	485	2	US-08-811-897A-17	Sequence 17, Appl			
14	1151.5	49.2	485	2	US-08-855-213-17	Sequence 17, Appl			
15	1151.5	49.2	485	4	US-09-201-474-17	Sequence 17, Appl			
16	1150	49.1	525	2	US-08-811-897A-23	Sequence 23, Appl			
17	1150	49.1	525	2	US-08-855-213-23	Sequence 23, Appl			
18	1150	49.1	525	4	US-09-201-474-23	Sequence 23, Appl			
19	1144.5	48.9	448	2	US-08-811-897A-22	Sequence 22, Appl			
20	1144.5	48.9	448	2	US-08-855-213-22	Sequence 22, Appl			
21	1144.5	48.9	448	4	US-09-201-474-22	Sequence 22, Appl			
22	1143.5	48.8	448	2	US-08-811-897A-18	Sequence 18, Appl			
23	1143.5	48.8	448	2	US-08-855-213-18	Sequence 18, Appl			
24	1143.5	48.8	448	4	US-09-201-474-18	Sequence 18, Appl			
25	1141.5	48.7	448	2	US-08-811-897A-16	Sequence 16, Appl			
26	1141.5	48.7	448	2	US-08-855-213-16	Sequence 16, Appl			
27	1141.5	48.7	448	4	US-09-201-474-16	Sequence 16, Appl			

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/538,816A

FILING DATE: 03-OCTOBER-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/437,466

FILING DATE: 09-MAY-1995

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-136 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 438 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: Human PACAP/VIP R-2

HYPOTHEetical: NO

US-08-538-816A-1

Query Match 99.5%; Score 2331; DB 2; Length 438;
Best Local Similarity 99.5%; Pred. No. 8.6e-212;
Matches 436; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIOBEETKCAELLRSQTEKHKACSGVWDNIT 60
DB 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIOBEETKCAELLRSQTEKHKACSGVWDNIT 60
QY 61 CWRPANVGETVTPCPKFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120
DB 61 CWRPANVGETVTPCPKFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120
QY 121 TFYILVKAITYTLGYSVLSLATSIIILCLFRKLHCTRYIHNLFLSFLTRALSIVLVD 180
DB 121 TFYILVKAITYTLGYSVLSLATSIIILCLFRKLHCTRYIHNLFLSFLTRALSIVLVD 180
QY 181 DVLYSSGTLHCPDPSSWVGCKLSLVFLOYCIWVNFLLVEGLYHLTLVAMLPERRC 240
DB 181 DVLYSSGTLHCPDPSSWVGCKLSLVFLOYCIWVNFLLVEGLYHLTLVAMLPERRC 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300
DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300
QY 301 SIIRILLOKLTSPDVGGNDOSQYKRLAKSTLILPLFGVHMVFAVFPPISSKYQILFE 360
DB 301 SIIRILLOKLTSPDVGGNDOSQYKRLAKSTLILPLFGVHMVFAVFPPISSKYQILFE 360
QY 361 LCLGSFQGLVAVLYCLFNSVQCELRKWRSCPTPSASRDYRVCGSSFRNGSEGALQ 420
DB 361 LCLGSFQGLVAVLYCLFNSVQCELRKWRSCPTPSASRDYRVCGSSFRNGSEGALQ 420
QY 421 FHRGSAQSFLOTETSVI 438
DB 421 FHRGSAQSFLOTETSVI 438

RESULT 2
US-09-076-651-1
; Sequence 1, Application US/09076651
; Patent No. 582899
; GENERAL INFORMATION:
; APPLICANT: Mojsov, Svetlana
; APPLICANT: Wei, Yang
; TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED
; TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/076,651
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/538,816
; FILING DATE: 03-OCTOBER-1995
; APPLICATION NUMBER: US 08/437,466
; FILING DATE: 09-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-136 CIP

TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Human PACAP/VIP R-2
HYPOTHETICAL: NO
US-09-076-651-1

Query Match 99.5%; Score 2331; DB 2; Length 438;
Best Local Similarity 99.5%; Pred. No. 8.6e-212;
Matches 436; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIOBEETKCAELLRSQTEKHKACSGVWDNIT 60
DB 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIOBEETKCAELLRSQTEKHKACSGVWDNIT 60
QY 61 CWRPANVGETVTPCPKFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120
DB 61 CWRPANVGETVTPCPKFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120
QY 121 TFYILVKAITYTLGYSVLSLATSIIILCLFRKLHCTRYIHNLFLSFLTRALSIVLVD 180
DB 121 TFYILVKAITYTLGYSVLSLATSIIILCLFRKLHCTRYIHNLFLSFLTRALSIVLVD 180
QY 181 DVLYSSGTLHCPDPSSWVGCKLSLVFLOYCIWVNFLLVEGLYHLTLVAMLPERRC 240
DB 181 DVLYSSGTLHCPDPSSWVGCKLSLVFLOYCIWVNFLLVEGLYHLTLVAMLPERRC 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300
DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300
QY 301 SIIRILLOKLTSPDVGGNDOSQYKRLAKSTLILPLFGVHMVFAVFPPISSKYQILFE 360
DB 301 SIIRILLOKLTSPDVGGNDOSQYKRLAKSTLILPLFGVHMVFAVFPPISSKYQILFE 360
QY 361 LCLGSFQGLVAVLYCLFNSVQCELRKWRSCPTPSASRDYRVCGSSFRNGSEGALQ 420
DB 361 LCLGSFQGLVAVLYCLFNSVQCELRKWRSCPTPSASRDYRVCGSSFRNGSEGALQ 420
QY 421 FHRGSAQSFLOTETSVI 438
DB 421 FHRGSAQSFLOTETSVI 438

RESULT 3
US-09-208-394-1
; Sequence 1, Application US/09208394
; Patent No. 6316596
; GENERAL INFORMATION:
; APPLICANT: Mojsov, Svetlana
; APPLICANT: Wei, Yang
; TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED
; TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/208,394
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/538,816
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-136 CIP
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human PACAP/VIP R-2
; HYPOTHETICAL: NO
; US-09-208-394-1

Query Match 99.5%; Score 2331; DB 4; Length 438;
Best Local Similarity 99.5%; Pred. No. 8.6e-212;
Matches 436; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MRTLPPALLTCWLLAPVNSIHPECRFHELEIQEETKCAELLRSQTEKHKACSGVMDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPECRFHELEIQEETKCAELLRSQTEKHKACSGVMDNIT 60

*Qy 61 CWRPANGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120
Db 61 CWRPANGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120

Qy 121 TFYILVKAITYLGYSVLSMLATGSIILCLFRKLHCTRYNIHLNLFILRAISVLVKD 180
Db 121 TFYILVKAITYLGYSVLSMLATGSIILCLFRKLHCTRYNIHLNLFILRAISVLVKD 180

Qy 181 DVLVSSSTGLHCPDQPSWVGCKLSLVFLOYCIMANFFWLLVEGLYHLLVAMLPVPRRC 240
Db 181 DVLVSSSTGLHCPDQPSWVGCKLSLVFLOYCIMANFFWLLVEGLYHLLVAMLPVPRRC 240

Qy 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSDVPWVIRIPILISIVNVLFI 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSDVPWVIRIPILISIVNVLFI 300

Qy 301 SIIRILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360
Db 301 SIIRILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360

Qy 361 LCLGSFQGLVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSFSRNGSEGALQ 420
Db 361 LCLGSFQGLVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSFSRNGSEGALQ 420

Qy 421 FHRGSAQSFLOTETSVI 438
Db 421 FHRASRAQSFLOTETSVI 438

RESULT 4
US-09-538-816A-9
; Sequence 9, Application US/08538816A
; Patent No. 5831051
; GENERAL INFORMATION:
; APPLICANT: Mojssov, Svetlana
; APPLICANT: Wei, Yang
;

; TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED
; TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE
; NUMBER OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Klauder & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/538,816A
; FILING DATE: 03-OCTOBER-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/437,466
; FILING DATE: 09-MAY-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-136 CIP
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 431 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human PACAP/VIP R-2B
; HYPOTHETICAL: NO
; US-08-538-816A-9

Query Match 95.6%; Score 2239.5; DB 2; Length 431;
Best Local Similarity 97.7%; Pred. No. 3.6e-203;
Matches 424; Conservative 2; Mismatches 3; Indels 5; Gaps 2;

Qy 5 LPPALLTCWLLAPVNSIHPECRFHELEIQEETKCAELLRSQTEKHKACSGVMDNITCWRP 64
Db 3 LGPSL---YLL--VNSIHPECRFHELEIQEETKCAELLRSQTEKHKACSGVMDNITCWRP 57

Qy 65 ANGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKITFYI 124
Db 58 ANGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKITFYI 117

Qy 125 LVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRYNIHLNLFILRAISVLVKDDVLY 184
Db 118 LVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRYNIHLNLFILRAISVLVKDDVLY 177

Qy 185 SSSGTLHCPDQPSWVGCKLSLVFLOYCIMANFFWLLVEGLYHLLVAMLPVPRRCFLAY 244
Db 178 SSSGTLHCPDQPSWVGCKLSLVFLOYCIMANFFWLLVEGLYHLLVAMLPVPRRCFLAY 237

Qy 245 LLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSDVPWVIRIPILISIVNVLFIISIR 304
Db 238 LLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSDVPWVIRIPILISIVNVLFIISIR 297

Qy 305 ILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFELCIG 364
Db 298 ILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFELCIG 357

Qy 365 SFQGLVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSFSRNGSEGALQFHRG 424
Db 365 SFQGLVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSFSRNGSEGALQFHRG 424
```

Db 358 SFQGLVAVLYCFLNSEVQCELKRWRSCTPTPSASRDYRVCGSSFSHNGSEGAQFHRA 417

QY 425 SRAQSFLQTETSVI 438

Db 418 SRAQSFLQTETSVI 431

RESULT 5

US-09-076-651-9

; Sequence 9, Application US/09076651

; Patent No. 5882899

; GENERAL INFORMATION:

; APPLICANT: Mojsov, Svetlana

; APPLICANT: Wei, Yang

; TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED

; TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE

; TITLE OF INVENTION: THEREOF

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klauber & Jackson

; STREET: 411 Hackensack Avenue

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/076,651

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/538,816

; FILING DATE: 03-OCTOBER-1995

; APPLICATION NUMBER: US 08/437,466

; FILING DATE: 09-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 600-1-136 CIP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201 487-5800

; TELEFAX: 201 343-1684

; TELEX: 133521

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 431 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; DESCRIPTION: Human PACAP/VIP R-2B

; HYPOTHETICAL: NO

US-09-076-651-9

Query Match 95.6%; Score 2239.5; DB 2; Length 431;

Best Local Similarity 97.7%; Pred. No. 3.6e-203;

Matches 424; Conservative 2; Mismatches 3; Indels 5; Gaps 2;

QY 5 LPBALLTCWLLAPVNSIHPECRFHLIEQEEETKCAELLRSQTEKHKACSGVWDNITCWRP 64

Db 3 LGPSU---YLL--VNSIHPECRFHLIEQEEETKCAELLRSQTEKHKACSGVWDNITCWRP 57

QY 65 ANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETPDPFDVACGYSDPDESKITFYI 124

Db 58 ANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETPDPFDVACGYSDPDESKITFYI 117

QY 125 LVKAIYTTGYSVLSMLATGSIILCLFKLHCTRYIHLNIFLSFILRAISVLVKDDVLY 184

Db 118 LVKAIYTTGYSVLSMLATGSIILCLFKLHCTRYIHLNIFLSFILRAISVLVKDDVLY 177

QY 185 SSSGTLHCPDQSSWVGCKLSLVELOYCIMANFFWLLVEGLYLAHTLLVAMLPRRRCFLAY 244

Db 178 SSSGTLHCPDQSSWVGCKLSLVELOYCIMANFFWLLVEGLYLAHTLLVAMLPRRRCFLAY 237

QY 245 LLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSDVPMWVIRIPILISIIIVNPFVLFISIR 304

Db 238 LLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSDVPMWVIRIPILISIIIVNPFVLFISIR 297

QY 305 ILLQKLTSPDVGGNDOSQYKRLAKSTLLIPLFGVHYMVFAVFPISISISKYQILFELCLG 364

Db 298 ILLQKLTSPDVGGNDOSQYKRLAKSTLLIPLFGVHYMVFAVFPISISISKYQILFELCLG 357

QY 365 SFQGLVAVLYCFLNSEVQCELKRWRSCTPTPSASRDYRVCGSSFSHNGSEGAQFHRA 424

Db 358 SFQGLVAVLYCFLNSEVQCELKRWRSCTPTPSASRDYRVCGSSFSHNGSEGAQFHRA 417

QY 425 SRAQSFLQTETSVI 438

Db 418 SRAQSFLQTETSVI 431

RESULT 6

US-09-208-394-9

; Sequence 9, Application US/09208394

; Patent No. 6316596

; GENERAL INFORMATION:

; APPLICANT: Mojsov, Svetlana

; APPLICANT: Wei, Yang

; TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED

; TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE

; TITLE OF INVENTION: THEREOF

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klauber & Jackson

; STREET: 411 Hackensack Avenue

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/208,394

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/538,816

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 600-1-136 CIP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201 487-5800

; TELEFAX: 201 343-1684

; TELEX: 133521

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 431 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; DESCRIPTION: Human PACAP/VIP R-2B

; HYPOTHETICAL: NO

US-09-208-394-9

Query Match 95.6%; Score 2239.5; DB 4; Length 431;

Best Local Similarity 97.7%; Pred. No. 3.6e-203;
Matches 424; Conservative 2; Mismatches 3; Indels 5; Gaps 2;
QY 5 LPPALLTCLLAPVNSIHPECFHLEIOEETKCAELLRSQTEKHACSGWWDNITCWRP 64
DB 3 LQPSL---YLL--VNSIHPECFHLEIOEETKCAELLRSQTEKHACSGWWDNITCWRP 57
QY 65 ANVGETVTPCKVSNFYSKAGNISKNCTSDGSETPPDFVDACGSDPEDESKITFYI 124
DB 58 ANVGETVTPCKVSNFYSKAGNISKNCTSDGSETPPDFVDACGSDPEDESKITFYI 117
QY 125 LVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRYIHNLFLSFILRAISVLVXDDVLY 184
DB 118 LVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRYIHNLFLSFILRAISVLVXDDVLY 177
QY 185 SSGTTLHCPDQSSWVGCKLSLVELOQYCI MANFFWLLVEGLYHLTLVAMLPDRCFLAY 244
DB 178 SSGTTLHCPDQSSWVGCKLSLVELOQYCI MANFFWLLVEGLYHLTLVAMLPDRCFLAY 237
QY 245 LLIGMLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISITVNFVLFISIR 304
DB 238 LLIGMLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISITVNFVLFISIR 297
QY 305 ILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYVMVFAVFPISISKYQILFELCIG 364
DB 298 ILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYVMVFAVFPISISKYQILFELCIG 357
QY 365 SFGGLVAVLYCFLNSEVOCELRKWRSCPTPSASRDYRVCGSFSRNGSEGALQFHRG 424
DB 358 SFGGLVAVLYCFLNSEVOCELRKWRSCPTPSASRDYRVCGSFSRNGSEGALQFHRG 417
QY 425 SRAQSFLOTETSVI 438
DB 418 SRAQSFLOTETSVI 431
RESULT 7
US-08-538-816A-2
; Sequence 2, Application US/08538816A
; Patent No. 5831051
; GENERAL INFORMATION:
; APPLICANT: Mojsov, Svetlana
; APPLICANT: Wei, Yang
; TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED
; TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/538,816A
; FILING DATE: 03-OCTOBER-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/437,466
; FILING DATE: 09-MAY-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-136 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684
TELEX: 133521
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: RPACAP-3/RVIP-2
; HYPOTHETICAL: NO
; US-08-538-816A-2
Query Match 86.7%; Score 2030; DB 2; Length 437;
Best Local Similarity 87.4%; Pred. No. 2.2e-183;
Matches 373; Conservative 23; Mismatches 31; Indels 0; Gaps 0;
QY 12 CWLLAPVNSIHPECFHLEIOEETKCAELLRSQTEKHACSGWWDNITCWRPANVGETV 71
DB 11 CWLLVRVSSIHPECFHLEIOEETKCAELLSSQTEHQACSGWWDNITCWRPADVGETV 70
QY 72 TVPCPKVSNFYSKAGNISKNCTSDGSETPPDFVDACGSDPEDESKITFYILKAIYT 131
DB 71 TVPCPKVSNFYSKAGNISKNCTSDGSETPPDFVDACGSDPEDESKITFYILKAIYT 130
QY 132 LGYSVLSMLATGSIILCLFRKLHCTRYIHNLFLSFILRAISVLVXDDVLYSSSGTLLH 191
DB 131 LGYSVLSMLATGSIILCLFRKLHCTRYIHNLFLSFILRAISVLVXDDVLYSSSGTLLH 190
QY 192 CPDQSSWVGCKLSLVELOQYCI MANFFWLLVEGLYHLTLVAMLPDRCFLAYLLHGMGL 251
DB 191 CHDQPSWVGCKLSLVELOQYCI MANFFWLLVEGLYHLTLVAMLPDRCFLAYLLHGMGL 250
QY 252 PTVCGIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISITVNFVLFISIRILLOKLT 311
DB 251 PTVCGIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISITVNFVLFISIRILLOKLT 310
QY 312 SPDVGNDQSQYKRLAKSTLLIPLFGVHYVMVFAVFPISISKYQILFELCIGSFQGLV 371
DB 311 SPDVGNDQSQYKRLAKSTLLIPLFGVHYVMVFAVFPISISKYQILFELCIGSFQGLV 370
QY 372 AVLYCFLNSEVOCELRKWRSCPTPSASRDYRVCGSFSRNGSEGALQFHRGSRQAQSL 431
DB 371 AVLYCFLNSEVOCELRKWRGICLTQAGSRDYRLHWSMRNGSESAQIHRGSRQAQSL 430
QY 432 QTETSVI 438
DB 431 QSTSVI 437
RESULT 8
US-09-076-651-2
; Sequence 2, Application US/09076651
; Patent No. 5882899
; GENERAL INFORMATION:
; APPLICANT: Mojsov, Svetlana
; APPLICANT: Wei, Yang
; TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED
; TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/538,816A
; FILING DATE: 03-OCTOBER-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/437,466
; FILING DATE: 09-MAY-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-136 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800

;; CURRENT APPLICATION DATA: US/09/076,651
;; APPLICATION NUMBER: US/09/076,651
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/538,816
;; FILING DATE: 03-OCTOBER-1995
;; APPLICATION NUMBER: US 08/437,466
;; FILING DATE: 09-MAY-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 600-1-136 CIP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 437 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; DESCRIPTION: RPACAP-3/RVIP-2
;; HYPOTHETICAL: NO
;; US-09-076-651-2

Query Match 86.7%; Score 2030; DB 2; Length 437;
Best Local Similarity 87.4%; Pred. No. 2.2e-183;
Matches 373; Conservative 23; Mismatches 31; Indels 0; Gaps 0;
QY 12 CWLLAPVNSHPHPCRFHLEIQEBETKCAELLRSQTEKHKACSGVWDNITCWRPANVGETV 71
DB 11 CWLLVRVSSHPCRFHLEIQEBETKCAELLSSQTEKHKACSGVWDNITCWRPADVGETV 70
QY 72 TVPCPKVFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGSDPEDESKITFYILVKAITY 131
DB 71 TVPCPKVFSNFYSRPGNISKNCTSDGWSSETFPDFIDACGYNDPEDESKISFYILVKAITY 130
QY 132 LGYSVLSMSTATGIIICLFRKLHCTRNTHLNFLSFILRAISVLVKDVLVSSSGTLH 191
DB 131 LGYSVLSMSTTGTGIIICLFRKLHCTRNTHLNFLSFILRAISVLVKDVLVSSSGLLR 190
QY 192 CPDOPSSWVGCKLSLVFLQYCIMANFVLLVEGLYHLTLVAMLPFRRCFLAYLLIGWGL 251
DB 191 CHDOPASWVGCKLSLVFFQYCIMANFVLLVEGLYHLTLVAILPPSRCFLAYLLIGWGI 250
QY 252 PTVCGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIVNFVLFISIIRILLQKLT 311
DB 251 PSVCIGAWTATRLSLEDTCGWDNDHSPVWVIRIPILISIVNFVLFISIVRILLQKLT 310
QY 312 SPDVGNDQSQYKRLAKSTLLILPLFGVHYMVFAVFPISISSKYQILFELCLGSFQGLV 371
DB 311 SPDVGNDQSQYKRLAKSTLLILPLFGVHYMVFAVFPISISTYQILFELCVGSFQGLV 370
QY 372 AVLYCFNLSEVQCELRKRWRSRCPTPSASRDYRVCGSSFRNGSEGALQFHRGSRQSF 431
DB 371 AVLYCFNLSEVQCELRKRWRCGLCTQAGSRDYLHWSMSRNGSEGSALQIHRGSRQSF 430
QY 432 QTSVSI 438
DB 431 QTSVSI 437

RESULT 9
US-09-208-394-2
; Sequence 2, Application US/09208394
; Patent No. 6316596
; GENERAL INFORMATION:
; APPLICANT: Mojsov, Svetlana
; APPLICANT: Wei, Yang
; TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED

;; TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE
;; TITLE OF INVENTION: THEREOF
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Klauber & Jackson
;; STREET: 411 Hackensack Avenue
;; CITY: Hackensack
;; STATE: New Jersey
;; COUNTRY: USA
;; ZIP: 07601
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/208,394
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA: US 08/538,816
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 600-1-136 CIP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 437 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; DESCRIPTION: RPACAP-3/RVIP-2
;; HYPOTHETICAL: NO
;; US-09-208-394-2

Query Match 86.7%; Score 2030; DB 4; Length 437;
Best Local Similarity 87.4%; Pred. No. 2.2e-183;
Matches 373; Conservative 23; Mismatches 31; Indels 0; Gaps 0;
QY 12 CWLLAPVNSHPHPCRFHLEIQEBETKCAELLRSQTEKHKACSGVWDNITCWRPANVGETV 71
DB 11 CWLLVRVSSHPCRFHLEIQEBETKCAELLSSQTEKHKACSGVWDNITCWRPADVGETV 70
QY 72 TVPCPKVFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGSDPEDESKITFYILVKAITY 131
DB 71 TVPCPKVFSNFYSRPGNISKNCTSDGWSSETFPDFIDACGYNDPEDESKISFYILVKAITY 130
QY 132 LGYSVLSMSTATGIIICLFRKLHCTRNTHLNFLSFILRAISVLVKDVLVSSSGTLH 191
DB 131 LGYSVLSMSTTGTGIIICLFRKLHCTRNTHLNFLSFILRAISVLVKDVLVSSSGLLR 190
QY 192 CPDOPSSWVGCKLSLVFLQYCIMANFVLLVEGLYHLTLVAMLPFRRCFLAYLLIGWGL 251
DB 191 CHDOPASWVGCKLSLVFFQYCIMANFVLLVEGLYHLTLVAILPPSRCFLAYLLIGWGI 250
QY 252 PTVCGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIVNFVLFISIIRILLQKLT 311
DB 251 PSVCIGAWTATRLSLEDTCGWDNDHSPVWVIRIPILISIVNFVLFISIVRILLQKLT 310
QY 312 SPDVGNDQSQYKRLAKSTLLILPLFGVHYMVFAVFPISISSKYQILFELCLGSFQGLV 371
DB 311 SPDVGNDQSQYKRLAKSTLLILPLFGVHYMVFAVFPISISTYQILFELCVGSFQGLV 370
QY 372 AVLYCFNLSEVQCELRKRWRSRCPTPSASRDYRVCGSSFRNGSEGALQFHRGSRQSF 431
DB 371 AVLYCFNLSEVQCELRKRWRCGLCTQAGSRDYLHWSMSRNGSEGSALQIHRGSRQSF 430

ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/855,213
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,986
FILING DATE: 25-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, David S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 44168
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-855-213-19

Query Match 49.3%; Score 1153.5; DB 2; Length 467;
Best Local Similarity 49.7%; Pred. No. 1.3e-100;
Matches 226; Conservative 63; Mismatches 127; Indels 39; Gaps 6;

QY 10 LTCWLLAPVNSIHPCRFHLEIQEETKCAEL-----LRQTEKHKACSGVWNTICWR 63
DB 9 LTALLLPAVAMSHDCIF---KKEQAMCLERIORANDLMGLNESPSPGCPGMWNTICWK 64
QY 64 PANVGETVTVPCKVFSNF-----YSKAGNISKNCTSDGWSR 100
DB 65 PAQGVEMVLVSCPEVFRIFPDQVMTETIGDSGFADSNLSLEITDMGVVGRNCTEDGWSR 124
QY 101 TFPDFVACGYSD--PEDESKITFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTR 158
DB 125 PFPHYFACGFDDEPEPSGDQDYVYLSVKALYTVGYSTSLATLTAMVILCRFRKLHCTR 184
QY 159 NYTHLNLFLSILRAISLVKDDVLYSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFF 218
DB 185 NFTHMNLVFSFMLRAISLVKIDVLYAEQDSSHC---FVSTVECKAVMVFFHYCVSNYP 241
QY 219 WLLVEGLYLHTLLV-AMLPFRRCFLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDH 277
DB 242 WLFIEGLYLFTLLVETFPFERYFYWTIIGWGTPTVCVTVWVAVLRLYFDGACGWNDS 301
QY 278 SVPMWVIRIPILISITVNFVLFISIRILLOKUTSPDVGNDSQYKRLAKSTLLIPLF 337
DB 302 TALWVWIKGVPVGSIMVNFVLFIGIILVQLQSPDMGNGESSIYLRLARSTLLIPLF 361
QY 338 GVHYMFAVFPISISKYQILFELCLGSPQGLVAVLYCFNSEVQCELKRWRSRCP 397
DB 362 GIHTVFAFSPENVKRRLVFEGLGSGFGFVAVLYCFNLGEVQAEIRKRWRSWKVR 421
QY 398 SASRDYRVCGSSFRNGSEGALQPHRGSRAQSFQ 432
DB 422 YFTMDFKHPHSLASSGVNGTQLSLKSSQLR 456

RESULT 12
US-09-201-474-19
Sequence 19, Application US/09201474
Patent No. 639316
GENERAL INFORMATION:
APPLICANT: ONDA, Haruo
APPLICANT: OHTAKI, Tetsuya
APPLICANT: MASUDA, Yasushi
APPLICANT: KITADA, Chieko
APPLICANT: ISHIBASHI, Yoshihiro
APPLICANT: HOSoya, Masaki
APPLICANT: OGI, Kazuhiro
APPLICANT: MIYAMOTO, Yasunori
APPLICANT: HABAATA, Yugo
APPLICANT: SHIMAMOTO, No. 639931610
TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR PREPARING
TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/201,474
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/811,897
FILING DATE: 05-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, David S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 44168-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-201-474-19

Query Match 49.3%; Score 1153.5; DB 4; Length 467;
Best Local Similarity 49.7%; Pred. No. 1.3e-100;
Matches 226; Conservative 63; Mismatches 127; Indels 39; Gaps 6;

QY 10 LTCWLLAPVNSIHPCRFHLEIQEETKCAEL-----LRQTEKHKACSGVWNTICWR 63
DB 9 LTALLLPAVAMSHDCIF---KKEQAMCLERIORANDLMGLNESPSPGCPGMWNTICWK 64
QY 64 PANVGETVTVPCKVFSNF-----YSKAGNISKNCTSDGWSR 100
DB 65 PAQGVEMVLVSCPEVFRIFPDQVMTETIGDSGFADSNLSLEITDMGVVGRNCTEDGWSR 124
QY 101 TFPDFVACGYSD--PEDESKITFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTR 158
DB 125 PFPHYFACGFDDEPEPSGDQDYVYLSVKALYTVGYSTSLATLTAMVILCRFRKLHCTR 184
QY 159 NYTHLNLFLSILRAISLVKDDVLYSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFF 218
DB 185 NFTHMNLVFSFMLRAISLVKIDVLYAEQDSSHC---FVSTVECKAVMVFFHYCVSNYP 241
QY 219 WLLVEGLYLHTLLV-AMLPFRRCFLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDH 277
DB 242 WLFIEGLYLFTLLVETFPFERYFYWTIIGWGTPTVCVTVWVAVLRLYFDGACGWNDS 301
QY 278 SVPMWVIRIPILISITVNFVLFISIRILLOKUTSPDVGNDSQYKRLAKSTLLIPLF 337
DB 302 TALWVWIKGVPVGSIMVNFVLFIGIILVQLQSPDMGNGESSIYLRLARSTLLIPLF 361
QY 338 GVHYMFAVFPISISKYQILFELCLGSPQGLVAVLYCFNSEVQCELKRWRSRCP 397
DB 362 GIHTVFAFSPENVKRRLVFEGLGSGFGFVAVLYCFNLGEVQAEIRKRWRSWKVR 421
QY 398 SASRDYRVCGSSFRNGSEGALQPHRGSRAQSFQ 432
DB 422 YFTMDFKHPHSLASSGVNGTQLSLKSSQLR 456

RESULT 13
US-08-811-897A-17
Sequence 17, Application US/08811897A
Patent No. 5858787
GENERAL INFORMATION:
APPLICANT: ONDA, Haruo
APPLICANT: OHTAKI, Tetsuya
APPLICANT: MASUDA, Yasushi
APPLICANT: KITADA, Chieko
APPLICANT: ISHIBASHI, Yoshihiro
APPLICANT: HOSoya, Masaki
APPLICANT: OGI, Kazuhiro
APPLICANT: MIYAMOTO, Yasunori
APPLICANT: HABAATA, Yugo
APPLICANT: SHIMAMOTO, No. 585878710


```

/ TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR PREPARING
/ TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF
/ NUMBER OF SEQUENCES: 56
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
/ ADDRESSEE: CUSHMAN
/ STREET: 130 Water Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: US
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/811,897A
/ FILING DATE: 05-MAR-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/202,986
/ FILING DATE: February 25, 1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: RESNICK, David S.
/ REGISTRATION NUMBER: 34235
/ REFERENCE/DOCKET NUMBER: 44168-DIV
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)523-3400
/ TELEFAX: (617)523-6440
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 485 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-811-897A-17

```

```

Query Match 49.2%; Score 1151.5; DB 2; Length 485;
Best Local Similarity 48.6%; Pred. No. 2.2e-100;
Matches 224; Conservative 72; Mismatches 126; Indels 39; Gaps 6;

QY 1 MRTLPPALLTCWLLAPVNSIHPCRFHLEIQEETKCAEL-----LRSQTEKHKACSG 54
Db 18 MASTAQVSLAALLPMLPATAHSDCIF---KKEQAMCLEKIQRVNDLMLGNDSSPGCPG 73

QY 55 VWDNITCWRPANVGSTVTPCPKVSFNF-----YSKAGNISK 91
Db 74 MWDNITCWRPANVGSTVTPCPKVSFNF-----YSKAGNISK 133

QY 92 NCTSDGWSSETPFDVADAGYSDPEDES--KITFYLLKAIYTLGYSVLSLMSLATGSIILC 149
Db 134 NCTEDGWSSEFPFHYFDACGFEEYSESTGDDYYLKVSLVGYSTSLVTLTTAMVILC 193

QY 150 LFRKLHCTRYNIHLNLFILRAISVLVKDDVLYSSSGTHICPDQSSWVGCKSLVFL 209
Db 194 RFRKLHCTRYNIHLNLFILRAISVLVKDDVLYSSSGTHICPDQSSWVGCKSLVFL 209

QY 210 QYICMANPFWLLVEGLYLLHTLLV-AMLPFRCLAYLLIGLPTVCIGAMTAARLYLED 268
Db 251 HCVVSNVFWLFIKGLYLLHTLLVETFFPERFYFYIIGGTFTVCVSWAMRLYLED 310

QY 269 TGCWDTNDSVFWVWIRIPILISIVNLFVLSIRILLOKLTSPDVGNDQSQYKRLAK 328
Db 311 TGCWDMNDNTALWVVIKGVVGSIMVNFVLIIGIIVLVQKLSQDMGNESSIYRLAR 370

QY 329 STLLLLPLFGVHYVYAFVPIISISKYQILLCIGSQGLVAVLYCFINSEVQCELRK 388
Db 371 STLLLLPLFGHYTHVAFSPNVSRKRLVFLGLGFSQGFVAVLYCFINSEVQAEIKR 430

QY 389 KWRSCRPTSPSRDYRVCGSSFSRNGSGALQFHRGSAQS 429
Db 431 KWRSKVNRVYTMDEKRRHPSIASSGVNGGTQLSILSKSS 471

```

```

RESULT 14
US-08-855-213-17
/ Sequence 17, Application US/08855213
/ Patent No. 5892004
/ GENERAL INFORMATION:
/ APPLICANT: ONDA, Haruo
/ APPLICANT: OHTAKI, Tetsuya
/ APPLICANT: MASUDA, Yasushi
/ APPLICANT: KITADA, Chieko
/ APPLICANT: ISHIBASHI, Yoshihiro
/ APPLICANT: HOSoya, Masaki
/ APPLICANT: OGI, Kazuhiro
/ APPLICANT: MIYAMOTO, Yasunori
/ APPLICANT: HABATA, Yugo
/ APPLICANT: SHIMAMOTO, No. 5892004io
/ TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR
/ TITLE OF INVENTION: PREPARING SAID PROTEIN, AND USE THEREOF
/ NUMBER OF SEQUENCES: 55
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
/ ADDRESSEE: CUSHMAN
/ STREET: 130 Water Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: US
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/855,213
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/202,986
/ FILING DATE: 25-FEB-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: RESNICK, David S.
/ REGISTRATION NUMBER: 34235
/ REFERENCE/DOCKET NUMBER: 44168
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)523-3400
/ TELEFAX: (617)523-6440
/ TELETYPE: 200291 STRE UR
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 485 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-855-213-17

```

```

Query Match 49.2%; Score 1151.5; DB 2; Length 485;
Best Local Similarity 48.6%; Pred. No. 2.2e-100;
Matches 224; Conservative 72; Mismatches 126; Indels 39; Gaps 6;

QY 1 MRTLPPALLTCWLLAPVNSIHPCRFHLEIQEETKCAEL-----LRSQTEKHKACSG 54
Db 18 MASTAQVSLAALLPMLPATAHSDCIF---KKEQAMCLEKIQRVNDLMLGNDSSPGCPG 73

QY 55 VWDNITCWRPANVGSTVTPCPKVSFNF-----YSKAGNISK 91
Db 74 MWDNITCWRPANVGSTVTPCPKVSFNF-----YSKAGNISK 133

QY 92 NCTSDGWSSETPFDVADAGYSDPEDES--KITFYLLKAIYTLGYSVLSLMSLATGSIILC 149
Db 134 NCTEDGWSSEFPFHYFDACGFEEYSESTGDDYYLKVSLVGYSTSLVTLTTAMVILC 193

QY 150 LFRKLHCTRYNIHLNLFILRAISVLVKDDVLYSSSGTHICPDQSSWVGCKSLVFL 209

```

Db 194 RFRKLCTRNFIHMLNFVSMFLRAISVFIKDWLLIYAEQDSNHC---FVSTVECKAVWVFF 250
QY 210 QYCI MANFWLLVEGLYLHTLLV-AMLPFRRCFLAYLLIGWGLPTVCIGAWTAARLYLED 268
Db 251 HVCVSNYFWLFTGLYLFLLVETFPFRRYFYWIIIGWGTPTCVSVWAMLRYFDD 310
QY 269 TGCWDTNDHSPVWVIRIPILISIIIVNFVLFISIIRILLLOKLTSPDVGGNDQOYKRLAK 328
Db 311 TGCWMDNDTALMWVVKPGVGSIMVNFVFIIGIIVLVQKLSQSPDMGNGNESSIYLRAR 370
QY 329 STLLPLFGVHYMVFAPFPISSKYQILFELCLGSGFQGLVAVLYCFNLSEVQCELKR 388
Db 371 STLLPLFGIHYTVFAFSPENVSKRERLVFELGLSGFQGFVAVLYCFNLSEVQAEIKR 430
QY 389 KWSRCPTPSASRDYRVCSSFRNGSEGALQPHRGSRAS 429
Db 431 KWSRWKNRYFTMDFKHRHPSLASSGVNGGTQLSILSKSS 471

RESULT 15

US-09-201-474-17
; Sequence 17, Application US/09201474
; Patent No. 6399316
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSoya, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HAKATA, Yugo
; APPLICANT: SHIMAMOTO, No. 639931610
; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR PREPARING
; TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201,474
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/811,897
; FILING DATE: 05-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-201-474-17

Query Match 49.2%; Score 1151.5; DB 4; Length 485;
Best Local Similarity 48.6%; Pred. No. 2.2e-100;
Matches 224; Conservative 72; Mismatches 126; Indels 39; Gaps 6;
QY 1 MRTLPPALLTCWLLAPVNSIIHPECRFHELEIOBEETKCAEL-----LRSQTEKHKACSG 54
Db 18 MASIAQVSLAALLLPMATAMHSDCIF---KREQAMCLEKIQRVNDLMGLNDSSPGCPG 73
QY 55 VNDNITCWPANVGETVTVPCKVFSNF-----YSKAGNISK 91
Db 74 MNDNITCWPANVGENVLSVCPFLFNPDOVWETETIGFADFADSKSLDLSDMRVSR 133
QY 92 NCTSDGMSSETFDPVDACGSDPEDES--KITFYILLVKAITYLGYSVLSMATGSIILC 149
Db 134 NCTEDGMSSETFPHYFACGFEEYSESTGDDYYILSVKALYTVGYSTSLVTTTAMVILC 193
QY 150 LFRKLCTRNFIHMLNFVSMFLRAISVFIKDWLLIYAEQDSNHC---FVSTVECKAVWVFF 209
Db 194 RFRKLCTRNFIHMLNFVSMFLRAISVFIKDWLLIYAEQDSNHC---FVSTVECKAVWVFF 250
QY 210 QYCI MANFWLLVEGLYLHTLLV-AMLPFRRCFLAYLLIGWGLPTVCIGAWTAARLYLED 268
Db 251 HVCVSNYFWLFTGLYLFLLVETFPFRRYFYWIIIGWGTPTCVSVWAMLRYFDD 310
QY 269 TGCWDTNDHSPVWVIRIPILISIIIVNFVLFISIIRILLLOKLTSPDVGGNDQOYKRLAK 328
Db 311 TGCWMDNDTALMWVVKPGVGSIMVNFVFIIGIIVLVQKLSQSPDMGNGNESSIYLRAR 370
QY 329 STLLPLFGVHYMVFAPFPISSKYQILFELCLGSGFQGLVAVLYCFNLSEVQCELKR 388
Db 371 STLLPLFGIHYTVFAFSPENVSKRERLVFELGLSGFQGFVAVLYCFNLSEVQAEIKR 430
QY 389 KWSRCPTPSASRDYRVCSSFRNGSEGALQPHRGSRAS 429
Db 431 KWSRWKNRYFTMDFKHRHPSLASSGVNGGTQLSILSKSS 471

Search completed: June 22, 2004, 09:00:09
Job time : 25 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 22, 2004, 08:54:08 ; Search time 45 Seconds
(without alignments)
3071.044 Million cell updates/sec

Title: US-09-983-000a-20
Perfect score: 2342
Sequence: 1 MRTLPPALLTCWLLAPVNS.....LQFHGRSAQSFLETSTVI 438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_plant:*
- 10: sp_rodent:*
- 11: sp_virus:*
- 12: sp_vertebrate:*
- 13: sp_unclassified:*
- 14: sp_rviro:*
- 15: sp_bacteriap:*
- 16: sp_archaeap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1324	56.5	426	13 Q802T6	Q802t6 fugu rubrip
2	1151	49.1	459	11 Q8BGA4	Q8bga4 mus musculus
3	1141.5	48.7	444	13 Q3VHC6	Q3vhc6 rana ridibu
4	1126	48.1	496	11 Q8BLT3	Q8blt3 mus musculus
5	1124	48.0	465	13 Q9PTK1	Q9ptk1 xenopus lae
6	1114.5	47.6	455	13 Q30Y10	Q30y10 rana ridibu
7	1100	47.0	418	13 Q31BG2	Q31bg2 gallus gall
8	1099	46.9	434	13 Q802T7	Q802t7 fugu rubrip
9	1092	46.6	480	13 Q30Y07	Q30y07 rana ridibu
10	1090	46.5	465	13 Q73769	Q73769 carassius a
11	1084.5	46.3	495	13 Q90Y08	Q90y08 rana ridibu
12	1059	45.2	419	13 Q8AXV3	Q8axv3 fugu rubrip
13	1056.5	45.1	465	13 Q30Y09	Q30y09 rana ridibu
14	1041	44.4	419	13 Q8AXV4	Q8axv4 fugu rubrip
15	1020.5	43.6	374	6 Q8WMR0	Q8wmr0 ovis aries
16	1003.5	42.8	528	4 Q81V17	Q81v17 homo sapien

17	996.5	42.5	402	6 Q8WMO9	Q8wmq9 ovis aries
18	971.5	41.5	438	13 Q73768	Q73768 carassius a
19	939	40.1	438	13 Q8AXV2	Q8axv2 fugu rubrip
20	876	37.4	423	6 Q9N1F8	Q9n1f8 bos taurus
21	872	37.2	439	11 Q9WU99	Q9wu99 rattus norv
22	870	37.2	441	6 Q8TUJ0	Q8tuj0 bos taurus
23	870	37.1	423	6 Q9BDH9	Q9bdh9 bos taurus
24	846.5	36.1	404	6 Q9TUI1	Q9tui1 bos taurus
25	844.5	36.1	407	6 Q9BDI0	Q9bdi0 ovis aries
26	764	32.6	595	6 Q9TUI3	Q9tui3 canis famli
27	760.5	32.5	542	13 Q9PVD2	Q9pvd2 brachydanio
28	756.5	32.3	591	11 Q91WV4	Q91wv4 mus musculu
29	754.5	32.2	589	6 Q7YRI3	Q7yri3 cervus elap
30	754.5	32.2	591	11 Q80WU8	Q80wu8 mus musculu
31	747	31.9	536	13 Q9PVD3	Q9pvd3 brachydanio
32	723.5	30.9	359	4 Q9HB45	Q9hb45 homo sapien
33	707	30.2	621	4 Q8N429	Q8n429 homo sapien
34	688	29.4	575	13 Q9PWB7	Q9pwb7 brachydanio
35	684.5	29.2	546	11 Q91V95	Q91v95 mus musculu
36	681.5	29.1	490	13 Q8UUV5	Q8uvy5 xenopus lae
37	681.5	29.1	492	13 Q9PUK1	Q9puk1 hoplobatr
38	673	28.7	489	13 Q8UYV4	Q8uyv4 rana pipien
39	668.5	28.5	455	4 Q86X15	Q86x15 homo sapien
40	652.5	27.9	512	11 Q80YA1	Q80yal mus musculu
41	648	27.7	485	11 Q8K0B5	Q8k0b5 mus musculu
42	622.5	26.6	409	4 Q86YG9	Q86ygg homo sapien
43	509	21.7	168	13 Q9YHC7	Q9yhc7 rana ridibu
44	501	21.4	445	13 Q98UC2	Q98uc2 ameiriurus ne
45	495	21.1	437	6 Q8WML8	Q8wml8 tupaia bela

ALIGNMENTS

RESULT 1

Q802T6
ID Q802T6 PRELIMINARY; PRT; 426 AA.
AC Q802T6;
DT 01-JUN-2003 (TREMREL. 24, Created)
DT 01-JUN-2003 (TREMREL. 24, Last sequence update)
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE Vasoactive intestinal peptide receptor.
GN VIPR2B.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Cardoso J.C.R., Power D.M., Elgar G., Clark M.S., Canario A.V.M.;
RT "Isolation and characterisation of the secretin receptor family
RT members in Fugu rubripes.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ408878; CAC83861.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004873; F:receptor activity; IEA.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; HormR; 1.
DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 426 AA; 48447 MW; 9D8C4AABF407E92A CRC64;

Query Match 56.5%; Score 1324; DB 13; Length 426;
Best Local Similarity 58.8%; Pred. No. 2.5e-112;
Matches 245; Conservative 62; Mismatches 104; Indels 6; Gaps 3;

```

Best Local Similarity 49.5%; Pred. No. 1.6e-96;
Matches 225; Conservative 66; Mismatches 124; Indels 40; Gaps 7;

QY 22 HPCRFLHLETOEBETKCAELLRQTEKHKACGWDNITCWRPANVGETVTVPCPKVFSN 81
Db 16 HPCNLFLEVERDHAELRLREEKEATSRKGVWDSIACWERAEGEIVTIPCPRVLKT 75
QY 82 FYSKAGNISKNCTSDGWSFPPFDVADAGYSDPEDSKITFYILVKAIYTLGYSVLSMSL 141
Db 76 VFRNGNISRNCTSGAGSDIFPNMTSVCGSNTSQDKVRLFYVQVTLVYLGHSLSIAL 135
QY 142 ATGSIILCLFRKLHCTRNHYHLNLFSLFRLRAISLVKDDVLYSSSSTLHCPQPSWVG 201
Db 136 ITGSAVLCLFRKLHCTRNHYHLNLFSLFRLRAISLVKDDVLYSSSSTLHCPQPSWVG 192
QY 202 CKLSLVFLQVCIMANFVLLVGLYHLTLVAMLPFRCLFAYLLIGWGLPTVCIGAWTA 261
Db 193 CKTSLVFFQYFIWANFVLLVGLYHLTLVAMLPFRCLFAYLLIGWGLPTVCIGAWTA 252
QY 262 ARYLEDTGWDNDHSDVPMWVIRIPILISIIIVNFVLFISIRILLOKLTSPDVGGNDQS 321
Db 253 MRYILEDTGWDNDHSDVPMWVIRIPILISIIIVNFVLFISIRILLOKLTSPDVGGNDQS 312
QY 322 QYRELAKSTLLILPLFGVHYVMFAVFPISISSKYQILFELCLGSGFQGLVAVLYCFNLSE 381
Db 313 QYRELAKSTLLILPLFGVHYVMFAVFPISISSKYQILFELCLGSGFQGLVAVLYCFNLSE 372
QY 382 VOCELKRWRSRCPSPASRDYRVCGSFSFNGSEGALQHRGSGRAQSFLOTETSVI 438
Db 373 LOVELKRWIRIMCLNAHLSGHH---SNTFTSGSELMAQSHRNSRAQSIMQSEITVL 426

RESULT 2
Q8BG44 PRELIMINARY; PRT; 459 AA.
ID Q8BG44 Q8BG44
AC Q8BG44 Q8BG44
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pituitary adenylate cyclase activating polypeptide type I receptor
DE precursor (Fragment).
GN ADCYAP1R1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK047304; BAC33020.1; -.
DR EMBL; AK081121; BAC38140.1; -.
DR PIR; PT0546; PT0698.
DR MGD; MGI:108449; Adcyap1r1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_4; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
DR NON_TER; 1.
SQ SEQUENCE 459 AA; 52407 MW; B0B49556988E96DA CRC64;

Query Match 49.1%; Score 1151; DB 11; Length 459;

Best Local Similarity 49.5%; Pred. No. 1.6e-96;
Matches 225; Conservative 66; Mismatches 124; Indels 40; Gaps 7;

QY 11 TCMLAPVN-SIHPCRFLHLETOEBETKCAEL-----LRSQTEKHKACGWDNITCWR 63
Db 1 TALLLLPMAIAMHSDCIF---KKEQAMCLRIQRANDLMGLNESSPGFCGMMDNITCWK 56
QY 64 PANVGTVTVPCPKVFSNF-----YSKAGNISKNCTSDGWS 100
Db 57 PAQIGEMVLVSCDEVFRINFDQVWMTETIGDSGFADNSLEITDMGVVGRNCTEDGWS 116
QY 101 TFPDFVADAGYSD--PEDESKITFYILVKAIYTLGYSVLSMSLATGSIILCLFRKLHCTR 158
Db 117 PPHYFDACGFDYEPESGDQDYVLSVKALYTVGYSTSLVTLTTAMVILCRPRKLHCTR 176
QY 159 NYTHMLNLFSLFRLRAISLVKDDVLYSSSSTLHCPQPSWVGCKLSLVFLQVCIMANEF 218
Db 177 NFTHMLNLFSLFRLRAISLVKDDVLYSSSSTLHCPQPSWVGCKLSLVFLQVCIMANEF 233
QY 219 WLLVEGLYHLTLV-AMLPFRCLFAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDH 277
Db 234 WLFIEGLYHLTLVETFEFFERRFYVWYTIIGWGTPTVCTVWAVLRYLFPDAGCWNDS 293
QY 278 SVPWVWVIRIPILISIIIVNFVLFISIRILLOKLTSPDVGGNDOSQYKRLAKSTLLILPLF 337
Db 294 TALWVWIKGVGSMVNFVLFISIRILLOKLTSPDVGGNDOSQYKRLAKSTLLILPLF 353
QY 338 GVHYVMFAVFPISISSKYQILFELCLGSGFQGLVAVLYCFNLSEVOCELKRWRSRCP 397
Db 354 GIHYTVFAFSPENVKRERLVFELGSGFGFVAVLYCFNLSEVOCELKRWRSRCP 413
QY 398 SASRDYRVCGSFSFNGSEGALQHRGSGRAQSFLO 432
Db 414 YFTWDFKRRHPSLASSGVNGTQLSILKSSQLR 448

RESULT 3
Q9YHC6 PRELIMINARY; PRT; 444 AA.
ID Q9YHC6 Q9YHC6
AC Q9YHC6 Q9YHC6
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vasoactive intestinal peptide/pituitary adenylate cyclase activating
DE polypeptide receptor.
OS Rana ridibunda (laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=99165178; PubMed=10067855;
RA Alexandre D., Anouar Y., Jegou S., Fournier A., Vaudry H.;
RT "A cloned frog vasoactive intestinal polypeptide/pituitary adenylate
RT cyclase-activating polypeptide receptor exhibits pharmacological and
RT tissue distribution characteristics of both VPAC1 and VPAC2 receptors
RT in mammals.";
RL Endocrinology 140:1285-1293 (1999).
DR EMBL; AF100644; AAD03602.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
DR NON_TER; 1.
SQ SEQUENCE 444 AA; 50955 MW; 883B25B729314C4C CRC64;

```

```

Query Match      48.7%; Score 1141.5; DB 13; Length 444;
Best Local Similarity 51.9%; Pred. No. 11e-95;
Matches 233; Conservative 65; Mismatches 128; Indels 23; Gaps 10;

QY 5 LPALLTCWLLAPVNSIIPEC--RHLEIQEETKCAELLRSQTEKKKACSGVNDNITCW 62
DB 4 LPALLCITGLSPILCVPEECSIMQIELKHCECVNHDYFNDT---AVCKETWNDNITCW 60

QY 63 RPANGETVTPCPKVFNSFYKA--GNISKNCTSDGMSCTPP-DFVACGYS--DPDE 117
DB 61 PSASIGEVVLQCPGYFNSFTTGTGTVNGVSKNCTSEGWSMYPATYAAACGFTNDTPT 120

QY 118 SKITFYILVKATYITLGYSVLSMSLATGSIILCLFKLHCTRYIHLNPLSFILRAISYL 177
DB 121 QQTVPFGATKTYTIGHSLSLSLSLAAMIIICIFRKLHCTRYIHLNPLSFILRAIAV 180

QY 178 VKDDVLYSSSGTLHCPDQPSWVGCKLSLVFTLQYICIMANFFVLLVEGLYLHTLLV-AMLP 236
DB 181 IKDIVLFSGESDHC---HVGSGVCKAAMVFQYICIMANFFVLLVEGLYLHLLVISF 237

QY 237 PRRCFLAYLLIGWLTVCIGAWTAARLYLEDTGCDTNDHVSFPWVIRIPILISILVNF 296
DB 238 EKKYFWWYIILGWGAPSVFITASLARVYFEDTGCWDTIESHL-WWIIKTPILVSLVNF 296

QY 297 VLFISITRILLOKLTSPDVGNDQSQYKELAKSTLLIPLFGVHYMVFAVEPISISSKYQ 356
DB 297 ILFICIRILVOKLHPDVGRENNSQYTRIAKSTLLIPLFGVHYIMFAFFDNPKEVK 356

QY 357 ILFELCLGSGFQGLVAVLYCFNLSEVQCELRKWRSCPTPSASRDYRVCSSFSRNGSE 416
DB 357 LVFELLILGSGFQGLVAVLYCFNLSEVQCELRKWRSCPTPSASRDYRVCSSFSRNGSE 416

QY 417 GALQFH-----RGSRAOSFIQTETSVI 438
DB 417 FSTQISMLTKCSPKTRCSCSF-QAEFSLV 444

RESULT 4
Q9BTL3 PRELIMINARY; PRT; 496 AA.
ID Q9BTL3
AC Q9BTL3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pituitary adenylate cyclase activating polypeptide type I receptor precursor.
DE precursor.
GN ADCYAP1R1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK042820; BAC31372.1;
DR PIR; PT0546; PT0698.
DR MGD; MGI:108449; Adcyap1r1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR InterPro; IPR000832; GPCR secretin.
DR Pfam; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm.2; 1.
DR Pfam; PF02793; HRM_1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.

```


[illegible][illegible]

```

RP SEQUENCE FROM N.A.
RC TISSUE=restis;
RA Alexandre D., Vaudry H., Carpentier V., Fournier A., Jegou S.,
AN Anuar Y.;
RT "Novel Splice Variants of Pituitary Adenylate Cyclase-Activating
RT Polypeptide Type I Receptor in Frog Exhibit Altered G-Protein
RT Coupling";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF312685; C:membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hoxmr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 480 AA; 55263 MW; 61A72A9CFB34104A CRC64;

Query Match 46.6%; Score 1092; DB 13; Length 480;
Best Local Similarity 46.3%; Pred. No. 4.1e-91;
Matches 219; Conservative 72; Mismatches 120; Indels 62; Gaps 10;

QY 9 LITCWLAPVNS-----IHPCRFLHEIQEETKCAEL-----LRSQTEKHKACSGWVDN 58
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 59
4 LRLVLLVAVSLMAYMHPYC---VIKKEETCLEKIQKLEWMNDSPGCGWMDN 59
QY 59 ITCWRPANVGETVTPCKVFS-----NFYSK-----AGNISKNCTSDGSETFPDFV 106
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 107
60 ITCWPAVVGKAVYIRCPAFWSMIDSDGMDFYDREHLEGVISRNCTENGSDFPHYS 119
QY 107 DACGY-----SDPEDESKITFYLVKAIYTLGYSVLSLMTSGSIILCLFRKLHCTRNVIH 162
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 163
120 DACGFDVNETGPDQD---TYLSVKALYTVGYSTSLVATTAMVILCFRKLHCTRNFIH 176
QY 163 LNFLSFILRAISLVKDDVLYSSGTHCPDQSSWGCKLSLVFLQYCYIMANFVLLV 222
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 223
177 MNLFVSFILRAISVRIKDEVLYAEQDSNHC---HVSTVECKAVMVFFYVCVMSNYFWLFI 233
QY 223 EGLYLHTLLV-AMLPPECELAYLLIGWGLPTVCIGAMTAARLYLEDGCDTNDHSVPW 281
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 282
234 EGLYLHTLLVETFFPERRYFYWTYTIIGMTPLCVTIWAVLRHDPDQGCWEMNNVALW 293
QY 282 WVIRIPILISIVNFPVLFISIRILLQKLTSPDVGNDQSQY----- 323
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 323
294 VWIKGFVIASIMINFLVFGIILVQKLPDIGNESSIYLCFQACFKRANQYSVKM 353
QY 324 -----KRLAKSTLLPLFGVHVWVFAVFPISISKYQILFELCLSGFQGLVAVLYC 376
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 376
354 SELSIITVRLARSTLLPLFGIHTVFAFSPENSVKRLVFLFELGLSGFQGFVAILYC 413
QY 377 FLNSVQCELRKKRSRCPSTPSASDRYVCGSFSRNGSEGALQPHRSRAQS 429
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 429
414 FLNGEVQSEIKRKRSWKVKNRYFAVDFKRRHPSLASSGVNGTQLSILSKSS 466

RESULT 10
O73769
ID O73769 PRELIMINARY; PRT; 465 AA.
AC O73769;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Pituitary adenylate cyclase activating polypeptide type 1
DE receptor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RA Wong A.O.L., Leung M.Y., Shea W.L.C., Chang J.P., Chow B.K.C.;
RT "Hypophyseotropic action of pituitary adenylate cyclase activating
RT polypeptide (PACAP) in the goldfish: immunohistochemical demonstration
RT of PACAP in the pituitary, PACAP stimulation of growth hormone release
RT from pituitary cells, and molecular cloning of pituitary type 1 PACAP
RT receptor.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF048820; AAC15699.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hoxmr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 465 AA; 53459 MW; 9779A95EDBD1DC1 CRC64;

Query Match 46.5%; Score 1090; DB 13; Length 465;
Best Local Similarity 54.6%; Pred. No. 6e-91;
Matches 209; Conservative 58; Mismatches 100; Indels 16; Gaps 8;

QY 17 PVNSIHPECFHLEIQEETKCAEL--LRSQTEKHK-ACSGWVDNITCWRPANVGETVTV 73
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 91
36 PIHSEISNC-----VIKKEERKCLELIALHDPNDGKFCPEWMDNLTCEATSVGKVVEV 91
QY 74 PCPKVFSNFYSK---AGNISKNCTSDGSETFPDFVDACGYSDPEDESKITFYLVKAIY 130
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 149
92 NCPFLF-DPNSPEBPGKISRNCITFCGWSSESYPHYVDACMIGENTTKPDM-YYASVKALY 149
QY 131 TLGYSVLSLMTSGSIILCLFRKLHCTRNVIHNLFLSFILRAISLVKDDVLYSSGTHL 190
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 209
150 TVGYSTSLVSLTTAMVILCFRKLHCTRNFIHMLFVSEMLRAISLVFIKQGLVAAEDSD 249
QY 191 HCPDQSSWGCKLSLVFLQYCYIMANFVLLVEGLYLHTLLV-AMLPPECEFLAYLLIGW 249
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 266
210 HCFVHT---VGCKAVMVFFHYCVMSNYFWLFIIEGLYFTLLVETFFPERRYFYWTYIIGW 266
QY 250 GLPTVCIGAMTAARLYLEDGCDTNDHSVPWVWVIRIPILISIVNFPVLFISIRILLQK 309
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 326
267 GTPTICVTIWAFLRHFDSDSCWMDNDNTALWVVIKGPVVASIMINFLVFIIGIILVQK 326
QY 310 LTPSDVCGNDOSQYKRLAKSTLLPLFGVHVWVFAVFPISISKYQILFELCLSGFQGL 369
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 386
327 LQSPDIGNESSIYRLARSTLLPLFGIHTVFAFSPENSVKRLVFLFELGLSGFQGF 386
QY 370 VVAVLYCFLNSEVQCELRKKRS 392
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 409
387 VVAVLYCFLNSEVQSEIKRKRS 409

RESULT 11
Q90Y08
ID Q90Y08 PRELIMINARY; PRT; 495 AA.
AC Q90Y08;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Pituitary adenylate cyclase-activating polypeptide receptor variant
DE PAC1-R41.
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```


DE Pituitary adenylate cyclase-activating polypeptide receptor variant
 DE PAC1-Rmc.
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Alexandre D., Vaudry H., Carpentier V., Fournier A., Jegou S.,
 RA Anouar Y.;
 RT "Novel Splice Variants of Pituitary Adenylate Cyclase-Activating
 RT Polypeptide Type I Receptor in Frog Exhibit Altered G-Protein
 RT Coupling";
 RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF312683; AAL26838.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR000832; GPCR secretin.
 DR InterPro; IPR001879; hormu_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
 KW Receptor.
 SQ SEQUENCE 465 AA; 53295 MW; E996B70A37DC23A9 CRC64;
 Query Match 45.1%; Score 1056.5; DB 13; Length 465;
 Best Local Similarity 50.8%; Pred. No. 6.8e-88;
 Matches 203; Conservative 64; Mismatches 96; Indels 37; Gaps 9;
 QY 9 LLTCWLLAPVNS-----IHPECRHLHIEQETKCAEL-----LRSQTEKHKACSGWDN 58
 DB 4 LLRLYLILLVASSILMAVMHPYC-----VIKBEETCLEKIQLELMWNDSMPGCGGMWDN 59
 QY 59 ITCWRPANGETVTPCPKVPES-----NFYSK-----AGNISKNCTSDGWSSTEDFV 106
 DB 60 ITCWMPAVGVKAVIRCAWFESMTDSEDGMPDYDREHLEGVISGNCENGSPPPHYS 119
 QY 107 DACGY----SDPEDESKITFYLVKAIYTLGYSLMSLATGSIILCLFRKLHCTRYIH 162
 DB 120 DACGFDVNETGDQD---TYFLSVKALYTVGYSTSLVATTAMVLCKRKLHCTRNFIH 176
 QY 163 LNLFLSFILRAISVLVDVLYSSSGTLHCDDQSSWGCKLSLVFLQYCTMANFFLLV 222
 DB 177 MNLFVSFILRAISVFIKDEVLYABQDSNHC---HVSTVEKAVMVFFHYCVMSNYFLFI 233
 QY 223 EGLYLHTLVV-AMLPERRCFRLAYLLIGWGLPTVCIGAWTAARLYLEDTCWDNDHVPW 281
 DB 234 EGLYLFTLVETFFPERFYFWYIILGWGLTPICVTIWAVLRHFDGCGWEMNNVALW 293
 QY 282 WVRIPILISIVNPLVFISIRILLQKLTGPDVGNDDQSQVKRIAKSTLLILPLFGVHY 341
 DB 294 WVIKGPVLASIMINFLVFLVFGIILVQKLQSPDIGNNESSYLRRLARSTLLILPLFGHY 353
 QY 342 MVFAVFPISISSKYQILFELCLGSGFQGLVAVLYCFLNSE 381
 DB 354 TVFAFSPENVSKRRLVFLGLGSGFQGLVAVLYCFLNGE 393

RESULT 14
 Q8AXV4 PRELIMINARY; PRT; 419 AA.
 ID Q8AXV4
 AC Q8AXV4
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DE Pituitary adenylate cyclase-activating polypeptide type 1 receptor
 DE Vasoactive intestinal peptide receptor.
 GN VIPR1B.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cardoso J.C.R., Power D.M., Canario A.V.M., Elgar G., Clark M.S.;
 RT "Isolation and characterisation of the VIPR/PACAP receptor gene family
 RT in Fugu rubripes";
 RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; A0296143; CAC82587.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR000832; GPCR secretin.
 DR InterPro; IPR001879; hormu_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
 KW Receptor.
 SQ SEQUENCE 419 AA; 47662 MW; 0B7A764B53BA2A7E CRC64;
 Query Match 44.4%; Score 1041; DB 13; Length 419;
 Best Local Similarity 50.5%; Pred. No. 1.6e-86;
 Matches 203; Conservative 60; Mismatches 125; Indels 14; Gaps 6;
 QY 25 CRFHEIQEETKCAELLRSQTEKHKACSGWDNIITCWRPANGETVTPCPK--VFSNF 82
 DB 2 CDMAELTEBEKDTCEAQENKT--AGCTGMDKITCWP SADVGVEVTPCPKLPFFSG 58
 QY 83 YSKAGNISKNCTSDGWSSTEDFVDAGY---SDPEDESKITFYLVKAIYTLGYSLMS 139
 DB 59 NTHLSNLKCTCTEDGWSPIIDYTEDCGYDFTNTVGDREAGFFSAIKVGYTVGHSVSLI 118
 QY 140 SLATGSIILCLFRKLHCTRYIHNLFLSILRAISVLVDVLYSSSGTLHCDDQSSW 199
 DB 119 SLTIGIILCLFRKLHCTRYIHNLFLSILRAISVLVDVLYSSSGTLHCDDQSSW 174
 QY 200 VGCKLSLVFLQYCTMANFFLLVEGLYHLLV-AMLPERRCFRLAYLLIGWGLTVCIGA 258
 DB 175 VGCKAVNAFPHYGIMASFFWLLVEGLYHLLVAVSFESERKYFWGYTILGWGAPSVISA 234
 QY 259 WTAARLYLEDTCWDNDHVPWVIRIPILISIVNPLVFISIRILLQKLTSPDVGNN 318
 DB 235 WVLTKAYLNDPGCWEIIDDTL-WWIIKTPILGTILVNFIPIRIIRILRQKNCPCDIGRR 293
 QY 319 DQSOYKRLAKSTLLILPLFGVHVMVFAVFPISISSKYQILFELCLGSGFQGLVAVLYCFL 378
 DB 294 ESHQYSLAKSTLLILPLFGVHVMVFAVFPISISSKYQILFELCLGSGFQGLVAVLYCFL 353
 QY 379 NSVQCEBKLRKWRSCRCPPTPSASRDYRVCGSGSFSRNGSEALQ 420
 DB 354 NGEVQAEIKRNRWRMLQRFGLGADTKYQPSIGSGNNGNFTSQ 395
 RESULT 15
 Q8WMRO PRELIMINARY; PRT; 374 AA.
 ID Q8WMRO
 AC Q8WMRO;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DE Pituitary adenylate cyclase-activating polypeptide type 1 receptor
 DE (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Search completed: June 22, 2004, 08:59:01
Job time : 47 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 22, 2004, 08:54:54 ; Search time 20 Seconds
(without alignments)
2106.594 Million cell updates/sec

Title: US-09-983-000A-20
Perfect score: 2342
Sequence: 1 MRTLPPALLTCWLLAPVNS.....LQHRGSRQAQSFLOQTETSVI 438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2342	100.0	438	2 G02822	vasoactive intesti
2	2032	86.8	437	2 S39069	vasoactive intesti
3	2030	86.7	437	2 JU0185	PACAP/VIP receptor
4	1153.5	49.3	467	2 JN0616	pituitary adenylat
5	1150	49.1	525	2 JN0902	pituitary adenylat
6	1129.5	48.2	495	2 S36114	pituitary adenylat
7	1129.5	48.2	495	2 S39061	pituitary adenylat
8	1127.5	48.1	513	2 S47631	pituitary adenylat
9	1115.5	47.6	523	2 S39060	pituitary adenylat
10	1084.5	45.5	459	2 JH0594	vasoactive intesti
11	1024	43.7	460	2 JG2194	vasoactive intesti
12	1018	43.5	495	2 JG2195	vasoactive intesti
13	997.5	42.6	449	2 S16319	secretin receptor
14	992.5	42.4	440	2 JG2532	secretin receptor
15	991	42.3	381	2 S33449	pituitary adenylat
16	879.5	37.6	423	2 A45363	somatoliberin rece
17	873.5	37.3	451	2 I46586	growth hormone-rel
18	846.5	36.1	423	2 S29753	growth hormone-rel
19	840.5	35.9	464	2 S29754	growth hormone-rel
20	760.5	32.5	585	2 A39286	parathyroid hormon
21	759	32.4	593	2 A49191	parathyroid hormon
22	754.5	32.2	591	2 S44203	parathyroid hormon
23	754.5	32.2	591	2 I54195	parathyroid hormon
24	738.5	31.5	589	2 I59297	parathyroid hormon
25	707	30.2	550	2 A57519	parathyroid hormon
26	701.5	30.0	462	2 JG2462	gastric inhibitory
27	688.5	29.4	455	2 I53273	gastric inhibitory
28	674.5	28.8	463	2 A46172	glucagon-like pept
29	670	28.6	466	2 S66676	glucose-dependent

30 669 28.6 466 2 G02234 gastric inhibitory
31 666.5 28.5 477 2 JC2041 glucagon receptor
32 657.5 28.1 463 2 S71624 glucagon-like pept
33 650.5 27.8 485 2 JQ1957 glucagon receptor
34 646.5 27.6 463 2 I84494 glucagon-like pept
35 646.5 27.6 491 2 I37411 glucagon-dependent
36 643 27.5 485 2 JC4363 glucagon receptor
37 489 20.9 415 2 S39535 corticotropin-rele
38 484 20.7 415 2 I58144 corticotropin-rele
39 483 20.6 431 2 I49279 sauvagine/corticot
40 482 20.6 411 2 A55610 corticotropin-rele
41 479 20.5 431 2 I49149 CRF receptor-mou
42 475.5 20.3 430 2 A56726 corticoliberin rec
43 459.5 19.6 444 2 A48260 corticoliberin rec
44 455.5 19.4 515 2 I49154 calcitonin recepto
45 447 19.1 482 2 A39285 calcitonin recepto

ALIGNMENTS

RESULT 1

G02822 vasoactive intestinal peptide receptor 2 - human

C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Jun-2000

C;Accession: G02822; JC2463
R;Lutz, E.M.
submitted to the EMBL Data Library, January 1996

A;Reference number: H01736

A;Accession: G02822

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-438 <LUT>

A;Cross-references: EMBL:X95097; NID:g1160469; PIDN:CAA64474.1; PID:g1160470
R;Svoboda, M.; Tastenoy, M.; Van Rampelbergh, J.; Goossens, J.F.; De Neef, P.; Waelbroe
Biochem. Biophys. Res. Commun. 205, 1617-1624, 1994

A;Title: Molecular cloning and functional characterization of a human VIP receptor from
A;Reference number: JC2463; MUID:95110300; PMID:7811244

A;Accession: JC2463
A;Molecule type: mRNA

A;Residues: 1-38, 'T', 40-411, 'H', 413-423, 'A', 425-438 <SVO>

A;Cross-references: GB:I36566; NID:G550477; PIDN:AC37569.1; PID:G550478

A;Experimental source: SUP-T1 lymphoblast cell line

C;Genetics:

A;Gene: GDB:VIPR2

A;Cross-references: GDB:335025

A;Map position: 7q36.3-7q36.3

C;Superfamily: Glucagon receptor

C;Keywords: Glycoprotein; intestine; receptor; transmembrane protein

F;130-150/Domain: transmembrane #status predicted <TM1>

F;160-179/Domain: transmembrane #status predicted <TM2>

F;206-228/Domain: transmembrane #status predicted <TM3>

F;241-262/Domain: transmembrane #status predicted <TM4>

F;282-304/Domain: transmembrane #status predicted <TM5>

F;329-349/Domain: transmembrane #status predicted <TM6>

F;361-384/Domain: transmembrane #status predicted <TM7>

F;58,88,92/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 2342; DB 2; Length 438;

Best Local Similarity 100.0%; Pred. No. 1.7e-186;

Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTLPPALLTCWLLAPVNSIHPECRPHLEIQEETKCAELLRSQTEKHKACSGWDNIT 60

Db 1 MRTLPPALLTCWLLAPVNSIHPECRPHLEIQEETKCAELLRSQTEKHKACSGWDNIT 60

Qy 61 CWRPNVGETVTPCPKVFNSFYSGKAGNISKNCTSDGSETFPDFVDACGSDPEDESKI 120

Db 61 CWRPNVGETVTPCPKVFNSFYSGKAGNISKNCTSDGSETFPDFVDACGSDPEDESKI 120

Qy 121 TFYLIVAKIYTLGVSYSLMSLATGSIILCLFRKLCHTRNYIHLNLFSLRAISVLVKD 180

Db 121 TFYLIVAKIYTLGVSYSLMSLATGSIILCLFRKLCHTRNYIHLNLFSLRAISVLVKD 180

Db 121 TFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRYIHNLFLSFILRAISVLVKD 180
Qy 181 DVLYSSGTLHCPDPQSSWGCKSLVFLQYICIMANFVLLVEGLYHLLVAMLPVRR 240
Db 181 DVLYSSGTLHCPDPQSSWGCKSLVFLQYICIMANFVLLVEGLYHLLVAMLPVRR 240
Qy 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIVNFVLI 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIVNFVLI 300
Qy 301 SIIRILLQKLTSPDVGNDQSOYKRLAKSTLLLLPLFGVHYVMVFAVFPISISSKYQLIFE 360
Db 301 SIIRILLQKLTSPDVGNDQSOYKRLAKSTLLLLPLFGVHYVMVFAVFPISISSKYQLIFE 360
Qy 361 LCLGSFQGLVAVLYCFLNSVQCELRKWRRCPTPSASRDYRVCGSSFRNGSEGLQ 420
Db 361 LCLGSFQGLVAVLYCFLNSVQCELRKWRRCPTPSASRDYRVCGSSFRNGSEGLQ 420
Qy 421 FHRGSRQSFLOTETSVI 438
Db 421 FHRGSRQSFLOTETSVI 438

RESULT 2
S39069
vasoactive intestinal peptide receptor VIP2 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 08-Oct-1999
C;Accession: J39069
R;Lutz, E.M.; Sheward, W.J.; West, K.M.; Morrow, J.A.; Fink, G.; Harmar, A.J.
FEBS Lett. 334, 3-8, 1993
A;Title: The VIP(2) receptor: molecular characterisation of a cDNA encoding a novel receptor
A;Reference number: S39069; MUID:94039806; PMID:8224221
A;Accession: J39069
A;Molecule type: mRNA
A;Residues: 1-437 <LUT>
A;Cross-references: EMBL:Z25885; NID:9414188; PIDN:CAA81104.1; PID:9414189
C;Superfamily: Glucagon receptor
C;Keywords: G protein-coupled receptor; intestine; transmembrane protein

Query Match 86.8%; Score 2032; DB 2; Length 437;
Best Local Similarity 87.4%; Pred. No. 8.3e-161;
Matches 373; Conservative 21; Mismatches 33; Indels 0; Gaps 0;
Qy 12 CWLLAPVNSIHPECRPHLEIQEETKCAELLRSQTEKHKACSGVMDNITCWRPANVGTV 71
Db 11 CWLLVRSSIHPECRPHLEIQEETKCAELLSSQENHRACSGVMDNITCWRPADIGTV 70
Qy 72 TVPCPKVFSNFYSKAGNISKNCTSDGWSSETFPDFVACGSDPDESKITFYILVKAIYT 131
Db 71 TVPCPKVFSNFYSRPGNISKNCTSDGWSSETFPDFIDACGYNDPDESKITFYILVKAIYT 130
Qy 132 LGYSVLSMLATGSIILCLFRKLHCTRYIHNLFLSFILRAISVLVKDDVLYSSGTLH 191
Db 131 LGYSVLSMLTGTGSIILCLFRKLHCTRYIHNLFLSFMLRAISVLVKDVLVSSGSLR 190
Qy 192 CPDOPSSWGCKSLVFLQYICIMANFVLLVEGLYHLLVAMLPVRRCFAYLLIGWL 251
Db 191 CHDQPSWGCKSLVFLQYICIMANFVLLVEGLYHLLVAILPPSRCLAYLLIGWI 250
Qy 252 PTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIVNFVLI FISTIRILLOKLT 311
Db 251 PSVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIVNFVLI FISTIRILLOKLT 310
Qy 312 SPDVGNDQSOYKRLAKSTLLLLPLFGVHYVMVFAVFPISISSKYQLIFECLGSFQGLV 371
Db 311 SPDVGNDQSOYKRLAKSTLLLLPLFGVHYVMVFAVFPISISSKYQLIFECLGSFQGLV 370
Qy 372 AVLYCFLNSVQCELRKWRRCPTPSASRDYRVCGSSFRNGSEGLQPHRGSRAQSF 431
Db 371 AVLYCFLNSVQCELRKWRRCPTPSASRDYRVCGSSFRNGSEGLQPHRGSRAQSF 430
Qy 432 QTETSVI 438
Db 431 QSETSVI 437

Db 431 QSETSVI 437
RESULT 3
JU0185
PACAP/VIP receptor (PACAPR-3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Nov-1999
C;Accession: A53471; JU0185
R;Inagaki, N.; Yoshida, H.; Mizuta, M.; Mizuno, N.; Fujii, Y.; Gonoi, T.; Miyazaki, J.;
Proc. Natl. Acad. Sci. U.S.A. 91, 2679-2683, 1994
A;Title: Cloning and functional characterization of a third pituitary adenylylate cyclase
A;Reference number: A53471; MUID:94195806; PMID:8146174
A;Accession: A53471
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-437 <RES>
A;Cross-references: GB:D28132; NID:9473721; PIDN:BAA05674.1; PID:9456376
A;Experimental source: strain C57BL/6
C;Superfamily: Glucagon receptor
C;Keywords: receptor

Query Match 86.7%; Score 2030; DB 2; Length 437;
Best Local Similarity 87.4%; Pred. No. 1.2e-160;
Matches 373; Conservative 23; Mismatches 31; Indels 0; Gaps 0;
Qy 12 CWLLAPVNSIHPECRPHLEIQEETKCAELLRSQTEKHKACSGVMDNITCWRPANVGTV 71
Db 11 CWLLVRSSIHPECRPHLEIQEETKCAELLSSQENHRACSGVMDNITCWRPADVGTV 70
Qy 72 TVPCPKVFSNFYSKAGNISKNCTSDGWSSETFPDFVACGSDPDESKITFYILVKAIYT 131
Db 71 TVPCPKVFSNFYSRPGNISKNCTSDGWSSETFPDFIDACGYNDPDESKITFYILVKAIYT 130
Qy 132 LGYSVLSMLATGSIILCLFRKLHCTRYIHNLFLSFILRAISVLVKDDVLYSSGTLH 191
Db 131 LGYSVLSMLTGTGSIILCLFRKLHCTRYIHNLFLSFMLRAISVLVKDVLVSSGSLR 190
Qy 192 CPDOPSSWGCKSLVFLQYICIMANFVLLVEGLYHLLVAMLPVRRCFAYLLIGWL 251
Db 191 CHDQPSWGCKSLVFLQYICIMANFVLLVEGLYHLLVAILPPSRCLAYLLIGWI 250
Qy 252 PTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIVNFVLI FISTIRILLOKLT 311
Db 251 PSVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIVNFVLI FISTIRILLOKLT 310
Qy 312 SPDVGNDQSOYKRLAKSTLLLLPLFGVHYVMVFAVFPISISSKYQLIFECLGSFQGLV 371
Db 311 SPDVGNDQSOYKRLAKSTLLLLPLFGVHYVMVFAVFPISISSKYQLIFECLGSFQGLV 370
Qy 372 AVLYCFLNSVQCELRKWRRCPTPSASRDYRVCGSSFRNGSEGLQPHRGSRAQSF 431
Db 371 AVLYCFLNSVQCELRKWRRCPTPSASRDYRVCGSSFRNGSEGLQPHRGSRAQSF 430
Qy 432 QTETSVI 438
Db 431 QSETSVI 437

RESULT 4
JN0616
pituitary adenylylate cyclase-activating polypeptide receptor 46-5 precursor - rat
N;Alternate names: PACAP receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C;Accession: JN0616; S36768
R;Hosoya, M.; Onda, H.; Ogi, K.; Masuda, Y.; Miyamoto, Y.; Ohtaki, T.; Okazaki, H.; Arin
Biochem. Biophys. Res. Commun. 194, 133-143, 1993
A;Title: Molecular cloning and functional expression of rat cDNAs encoding the receptor
A;Reference number: JN0616; MUID:93326107; PMID:7687425
A;Accession: JN0616
A;Molecule type: mRNA

F;78-525/Product: pituitary adenylate cyclase activating peptide receptor type I #statu
F;105,117,174,357,400,432/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 49.1%; Score 1150; DB 2; Length 525;
Best Local Similarity 48.2%; Pred. No. 1.4e-87;
Matches 225; Conservative 68; Mismatches 118; Indels 56; Gaps 7;

QY 12 CW-----LLAPNSIHPCRPHLEIQEETKCAELLRSOTE-----K 48
DB 52 CWPSPRYAGVVHVSLLAALLLPAPAMHSDCIF-----KKEQAMCLEKIQIANELMGFNDS 107
QY 49 HKACSGWMDNITCWRPANVGETVTPCPKVFNSF-----YSK 85
DB 108 SPGCPGMDNITCWPFAHGEVMVLVSCPFLFPNPDPQVWETIGESDFGDSNLSLDS 167
QY 86 AGNISKNCYSDGSETFPDPVDACGYSDPDES-----KITFYILVKAIYTLGYSVLSLSIAT 143
DB 168 MGVSRSNCTEDGSEPPHPHYFDACGPEYSESTGQDYVYLSVKALYTVGYSTSLVTLTT 227
QY 144 GSIIICLFRKLHCTRYHINLHLSFLSILRAISVLVKDDVLYSSGTLHCPDPQPSWVGCK 203
DB 228 AMVILCFRKLHCTRYHINLHLSFLSILRAISVLVKDDVLYSSGTLHCPDPQPSWVGCK 284
QY 204 LSLVFLQYCHMANFFMLLVLEGLYHILTV-AMLPRRRCFLAYLLIGWGLPTVCIGAWTAA 262
DB 285 AVWFFHYCVSVNFWLFIEGLYLTLLVETFFPERRYFYWYTIIGWGTPTVCVTWATL 344
QY 263 RLYLEDTCWDTNDHSVPWWIIRIPILISIIIVNFVLSIRILLOKLTSPDVCGNQSQ 322
DB 345 RLYFPDTCWDMNDSTALWWIIRIPILISIIIVNFVLSIRILLOKLTSPDVCGNQSQ 404
QY 323 YKRLAKSTLLIPLFGVHVVFVFPISISGKYQLFELCLGSGFQGLWAVLYCFNLSEV 382
DB 405 YLRLAKSTLLIPLFGHIVYVFAFSPENVSKRELVEFELGLSGFQGLWAVLYCFNLSEV 464
QY 383 QCEIKRWKRCPTPSADRYVCGVSFSGNSGALQFHRGSAQS 429
DB 465 QAEIKRWKRSWKVRYFAVDFKRRHPSLASSGVNGGTQLSTLSKSS 511

RESULT 6
S36114
pituitary adenylate cyclase-activating polypeptide type I receptor precursor - rat
N/Alternate names: PACAP receptor
C/Species: Rattus norvegicus (Norway rat)
C/Date: 06-Feb-1995 #sequence revision 06-Feb-1995 #text change 01-Dec-2000
C/Accession: S36114; JN0617; S39062; S39063; PN0608; PN0609; I58147; A48204
P/Morrow, J.A.; Eutz, E.M.; West, K.M.; Fink, G.; Harmar, A.J.
FEBS Lett. 329, 99-105, 1993
A/Title: Molecular cloning and expression of a cDNA encoding a receptor for pituitary
A/Reference number: S36114; MUID:93359075; PMID:8394834
A/Accession: S36114
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-495 <MOR>
A/Cross-references: EMBL:Z23282; NID:g397520; PIDN:CAA80820.1; PID:g397521
R/Hosoya, M.; Onda, H.; Ogi, K.; Masuda, Y.; Miyamoto, Y.; Ontaki, T.; Okazaki, H.; Ari
Biochem. Biophys. Res. Commun. 194, 133-143, 1993
A/Title: Molecular cloning and functional expression of rat cDNAs encoding the receptor
A/Reference number: JN0616; MUID:93326107; PMID:7687425
A/Accession: JN0617
A/Molecule type: mRNA
A/Residues: 1-495 <HOS>
A/Experimental source: brain
R/Spengler, D.; Waerber, C.; Pantaloni, C.; Holsboer, F.; Bockaert, J.; Seeburg, P.H.; C
Nature 365, 170-175, 1993
A/Title: Differential signal transduction by five splice variants of the PACAP receptor
A/Reference number: S36768; MUID:93382505; PMID:8396727
A/Accession: S39062
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-495 <SPE>
A/Cross-references: EMBL:Z23274; NID:g404220; PIDN:CAA80812.1; PID:g404221

A;Accession: S39063
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-348,350-495 <SP2>
A;Cross-references: EMBL:23275; NID:9404197; PIDN:CAA80813.1; PID:9404198
P;Svoboda, M.; Tastenoy, M.; Ciccarello, E.; Stievenart, M.; Christophe, J.
Biochem. Biophys. Res. Commun. 195, 881-888, 1993
A;Title: Cloning of a splice variant of the pituitary adenylate cyclase-activating polypeptide
A;Reference number: PN0608; MUID:93384616; PMID:8396930
A;Accession: PN0608
A;Molecule type: mRNA
A;Residues: 78-495 <SV0>
A;Accession: PN0609
A;Molecule type: protein
A;Residues: 349-376 <SV2>
R;Hashimoto, H.; Ishihara, T.; Shigemoto, R.; Mori, K.; Nagata, S.
Neuron 11, 333-342, 1993
A;Title: Molecular cloning and tissue distribution of a receptor for pituitary adenylate cyclase-activating polypeptide
A;Reference number: 158147; MUID:93357025; PMID:8394723
A;Accession: 158147
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-495 <RES>
A;Cross-references: GB:D16465; NID:9440381; PIDN:BA003932.1; PID:9457661
R;Pisegna, J.R.; Wank, S.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 6345-6349, 1993
A;Title: Molecular cloning and functional expression of the pituitary adenylate cyclase-activating polypeptide receptor
A;Reference number: A48204; MUID:93317678; PMID:8392197
A;Accession: A48204
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-420, 'L', 422-495 <PIS>
A;Cross-references: GB:L16680; NID:9347941; PIDN:AAA11792.1; PID:9347942
C;Comment: This protein stimulates both adenylate cyclase and phospholipase C and dually activates protein kinase C.
C;Superfamily: Glucagon receptor
C;Keywords: alternative splicing; anterior pituitary; G protein-coupled receptor; glycoprotein; hormone; pituitary; receptor; signal transduction; transmembrane protein
F;1-347,376-495/Product: pituitary adenylate cyclase-activating polypeptide receptor long form #1
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-495/Product: pituitary adenylate cyclase-activating polypeptide type I receptor #status predicted <TM1>
F;155-177/Domain: transmembrane #status predicted <TM1>
F;186-204/Domain: transmembrane #status predicted <TM2>
F;227-252/Domain: transmembrane #status predicted <TM3>
F;268-290/Domain: transmembrane #status predicted <TM4>
F;308-331/Domain: transmembrane #status predicted <TM5>
F;378-398/Domain: transmembrane #status predicted <TM6>
F;413-433/Domain: transmembrane #status predicted <TM7>
F;475,511,529,542,544/Binding site: carboxylate (Asn) (covalent) #status predicted
F;365,444/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 48.2%; Score 1129.5; DB 2; Length 495;
Best Local Similarity 46.8%; Pred. No. 6.5e-86;
Matches 226; Conservative 63; Mismatches 127; Indels 67; Gaps 7;
QY 10 LTCWLLAPVNSIHPCRFHLEIQBEETKCAEL-----LRSQTEKHKACSGVMDNITCWR 63
DB 9 LTALLPVAIAHMSDCIF----KKEQAMCLERIQANDLMGLNESPCCPGMWDNITCWK 64
QY 64 PANVGETVTPCPKVFNSF-----YSKAGNISKNCTSDGWS 100
DB 65 PAQVGEMLVSCPEVFRIFNPQVMMTETIGDSGFADNSLEITDMGVVGRNCTEDGWS 124
QY 101 TFPDFVDCGYSD--PEDESKITFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTR 158
DB 125 PFPHVFDACGDDYEPESGDQDYVLSVKALYTVGYSTSLATLTAMVILCRFKLHCTR 184
QY 159 NYIHNLFLSILRAISVLVKDDVLYSSSGTLHCPDQPSWVGKLSLVFLQYICIMANFF 218
DB 185 NFTHNMLFVSFMLRAISVFIKDWILYAEQDSHSC---FVSTVECKAVMVFHYCVVSNYF 241
QY 219 WLLVEGLYLHTLLV-AMLPFRRCFLAYLLIGLPTVCIGAWTAARLYLEDTCGWDNDH 277
DB 242 WLFIEGLYLTLVETFFPERRYFYWTIIIGWGTPTVCVTWAVLRLYFDDAGCWDNDS 301
QY 64 PANVGETVTPCPKVFNSF-----YSKAGNISKNCTSDGWS 100
DB 65 PAQVGEMLVSCPEVFRIFNPQVMMTETIGDSGFADNSLEITDMGVVGRNCTEDGWS 124
QY 101 TFPDFVDCGYSD--PEDESKITFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTR 158
DB 125 PFPHVFDACGDDYEPESGDQDYVLSVKALYTVGYSTSLATLTAMVILCRFKLHCTR 184
QY 159 NYIHNLFLSILRAISVLVKDDVLYSSSGTLHCPDQPSWVGKLSLVFLQYICIMANFF 218
DB 185 NFTHNMLFVSFMLRAISVFIKDWILYAEQDSHSC---FVSTVECKAVMVFHYCVVSNYF 241
QY 219 WLLVEGLYLHTLLV-AMLPFRRCFLAYLLIGLPTVCIGAWTAARLYLEDTCGWDNDH 277
DB 242 WLFIEGLYLTLVETFFPERRYFYWTIIIGWGTPTVCVTWAVLRLYFDDAGCWDNDS 301

QY 278 SVPWWVIRIPILISIIIVNFVLFISIRILLQKLTSPDVGGNDOSQY----- 323
DB 302 TALWWVVKGPVVGSMVNFVLFISIRILLQKLTSPDVGGNDOSQY----- 361
QY 324 -----KRLAKSTLLIPLFGVHYVMVFAVFPISISSKYQILFELCLGSGFQGL 369
DB 362 QHSCRKMSLSTTLRLARSTLLIPLFGHYTVFAFSPENVKRRLVFLGLGSGFQGF 421
QY 370 VVAVLYCFNLSEVOCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGALQFHRGSAQS 429
DB 422 VVAVLYCFNLSEVOCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGALQFHRGSAQS 481
QY 430 FLQ 432
DB 482 QLR 484
RESULT 7
S39061
Pituitary adenylate cyclase activating-peptide receptor form 3 - rat
N;Alternate names: PACAP receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
C;Accession: S39061
R;Spengler, D.; Waerber, C.; Pantaloni, C.; Holsboer, F.; Bockaert, J.; Seeburg, P.H.; J.
Nature 365, 170-175, 1993
A;Title: Differential signal transduction by five splice variants of the PACAP receptor
A;Reference number: S36768; MUID:93382505; PMID:8396727
A;Accession: S39061
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-495 <SPE>
A;Cross-references: EMBL:Z23273; NID:9404210; PIDN:CAA80811.1; PID:9404211
C;Superfamily: Glucagon receptor

Query Match 48.2%; Score 1129.5; DB 2; Length 495;
Best Local Similarity 46.8%; Pred. No. 6.5e-86;
Matches 226; Conservative 63; Mismatches 127; Indels 67; Gaps 7;
QY 10 LTCWLLAPVNSIHPCRFHLEIQBEETKCAEL-----LRSQTEKHKACSGVMDNITCWR 63
DB 9 LTALLPVAIAHMSDCIF----KKEQAMCLERIQANDLMGLNESPCCPGMWDNITCWK 64
QY 64 PANVGETVTPCPKVFNSF-----YSKAGNISKNCTSDGWS 100
DB 65 PAQVGEMLVSCPEVFRIFNPQVMMTETIGDSGFADNSLEITDMGVVGRNCTEDGWS 124
QY 101 TFPDFVDCGYSD--PEDESKITFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTR 158
DB 125 PFPHVFDACGDDYEPESGDQDYVLSVKALYTVGYSTSLATLTAMVILCRFKLHCTR 184
QY 159 NYIHNLFLSILRAISVLVKDDVLYSSSGTLHCPDQPSWVGKLSLVFLQYICIMANFF 218
DB 185 NFTHNMLFVSFMLRAISVFIKDWILYAEQDSHSC---FVSTVECKAVMVFHYCVVSNYF 241
QY 219 WLLVEGLYLHTLLV-AMLPFRRCFLAYLLIGLPTVCIGAWTAARLYLEDTCGWDNDH 277
DB 242 WLFIEGLYLTLVETFFPERRYFYWTIIIGWGTPTVCVTWAVLRLYFDDAGCWDNDS 301
QY 278 SVPWWVIRIPILISIIIVNFVLFISIRILLQKLTSPDVGGNDOSQY----- 323
DB 302 TALWWVVKGPVVGSMVNFVLFISIRILLQKLTSPDVGGNDOSQY----- 361
QY 324 -----KRLAKSTLLIPLFGVHYVMVFAVFPISISSKYQILFELCLGSGFQGL 369
DB 362 DLPVPDSQHSPPFLRLARSTLLIPLFGHYTVFAFSPENVKRRLVFLGLGSGFQGF 421
QY 370 VVAVLYCFNLSEVOCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGALQFHRGSAQS 429
DB 422 VVAVLYCFNLSEVOCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGALQFHRGSAQS 481
QY 430 FLQ 432


```

Db      482 QLR 484

RESULT 8
S47631
N;Alternate names: PACAP receptor
N;Contains: pituitary adenylate cyclase-activating polypeptide type I receptor long form
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C;Accession: S47631; S47632
R;Miyamoto, Y.; Habata, Y.; Ohkaki, T.; Masuda, Y.; Ogi, K.; Onda, H.; Fujino, M.
Biochim. Biophys. Acta 1218, 297-307, 1994
A;Title: Cloning and expression of a complementary DNA encoding the bovine receptor for
A;Reference number: S47631; MUID:94325336; PMID:8049255
A;Accession: S47631
A;Molecule type: mRNA
A;Residues: 1-513 <MIY>
A;Cross-references: EMBL:D17290; NID:g602765; PIDN:BA04122.1; PID:g1374682
A;Experimental source: brain
A;Accession: S47632
A;Molecule type: protein
A;Residues: 38-41,'X',43-50,'X',52-66 <MI2>
A;Experimental source: brain
C;Genetics:
A;Introns: 366/2
C;Function:
A;Description: stimulates both adenylate cyclase and phospholipase C
C;Superfamily: glucagon receptor
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; phosphoprotein
F;1-37/Domain: signal sequence #status predicted <SIG>
F;38-513/Product: pituitary adenylate cyclase-activating polypeptide type I receptor long
F;38-365,394-513/Product: pituitary adenylate cyclase-activating polypeptide type I rec
F;173-195/Domain: transmembrane #status predicted <TM1>
F;204-222/Domain: transmembrane #status predicted <TM2>
F;245-270/Domain: transmembrane #status predicted <TM3>
F;286-308/Domain: transmembrane #status predicted <TM4>
F;326-349/Domain: transmembrane #status predicted <TM5>
F;396-416/Domain: transmembrane #status predicted <TM6>
F;431-451/Domain: transmembrane #status predicted <TM7>
F;65,77,134,360,420/Binding site: carbonyl site: (Asn) (covalent) #status predicted
F;383,462/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match      48.1%; Score 1127.5; DB 2; Length 513;
Best Local Similarity 45.8%; Pred. No. 9.9e-86;
Matches 224; Conservative 72; Mismatches 126; Indels 67; Gaps 7;

QY      1 MRTLPPALLTCWLLAPVNSIHPECRHLELOBEETKCAEL-----LRSQTEKHKACSG 54
Db      18 MASTAQVSLAALLPLPMTAMHSDCIF---KKEQAMCLEKIORVNDLMDGLNDSPPGCPG 73
QY      55 VWDNITCWRPANVGETVTVPCKVFSNF-----YSKAGNISK 91
Db      74 MWDNITCWRPAHVGEMVLSVCPFLFRFPDQVWETIGFEGFADSKSLDLSDMRVSR 133
QY      92 NCTSDGWSFTPPDVCAGHSDPEDES--KITFYILVKAYITLGYSVLSMLATGSIILC 149
Db      134 NCTEDGWSFPPHYFDACGFEEYSESTGDDYYVLSVKALTYGVYSTLSVLTLTAMVILC 193
QY      150 LFRKLHCTRNYIHNLFLSFTLRAISVLVXDNDVLYSSSGTLHCPDQPSWVGKLSIVFL 209
Db      194 RFRKLHCTRNFIFHNLVFSVWMLRAISVFIKDWILYAEQDSNHC---FVSTVECKAVWVFF 250
QY      210 QYCIAMNFWMLVLEGLYHLTLV--AMLPPRCFLAYLLIGWGLPTVCIGAWTAARLYLED 268
Db      251 HYCVVSNFYFLFIEGLYFLTLVTFPPFRRYFYWYIIIGWGTPTVCVSVWAMRLRYFDD 310
QY      269 TGCWDTNDHSVPWVIRIPILISIVNFVLEFISIRILLQKLTSPDVGNDQSY----- 323
Db      311 TGCWDMNDNTALMWVIGPVVGSIMVNFVLFIGIIVLVQKLOSPDNGNGNESSYFCVQ 370
QY      324 -----KRLAKSTLLIPLFGVHWVFAVFPFISISKVOILFR 360

```

[illegible]

vasoactive intestinal peptide receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: JH0594; S56014
R: Ishihara, T.; Shigemoto, R.; Mori, K.; Takahashi, K.; Nagata, S.
Neuron 8, 811-819, 1992
A:Title: Functional expression and tissue distribution of a novel receptor for vasoactive intestinal peptide
A:Reference number: JH0594; MUID:92232309; PMID:1314625
A:Accession: JH0594
A:Molecule type: mRNA
A:Residues: 1-459 <ISH>
A:Cross-references: GB:M86835; NID:G207640; PIDN:AAA42331.1; PID:G207641
A:Experimental source: lung
R:Pei, L.; Melmed, S.
Biochem. J. 308, 719-723, 1995
A:Title: Characterization of the rat vasoactive intestinal polypeptide receptor gene 5'
A:Reference number: S56014; MUID:97104266; PMID:8948424
A:Accession: S56014
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-26 <PEI>
A:Cross-references: EMBL:U10635; NID:G505752; PIDN:AA848185.1; PID:G514311
C:Superfamily: Glucagon receptor
C:Keywords: G protein-coupled receptor; glycoprotein; intestine; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-459/Product: vasoactive intestinal polypeptide receptor #status predicted <MAT>
F:146-168/Domain: transmembrane #status predicted <TM1>
F:176-195/Domain: transmembrane #status predicted <TM2>
F:218-241/Domain: transmembrane #status predicted <TM3>
F:256-277/Domain: transmembrane #status predicted <TM4>
F:295-318/Domain: transmembrane #status predicted <TM5>
F:344-363/Domain: transmembrane #status predicted <TM6>
F:376-395/Domain: transmembrane #status predicted <TM7>
F:58,69,100,292/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 45.5%; Score 1064.5; DB 2; Length 459;
Best Local Similarity 47.1%; Pred. No. 1.5e-80;
Matches 221; Conservative 68; Mismatches 139; Indels 41; Gaps 11;
QY 1 MRTLPP-----ALLTCWLLAPVN-----SIHPECFHLEIOBEETKCAELLSQTE 47
Db 1 MRPPSPHVRWLCVLAGALAC-ALRPAGSOASPOHECYQLQIEFQRCQCLEBAQLENE 59
QY 48 HKACSGVNDNITCWRPANVGETVTPCPKFSNFYSKAG-NISKNCTSDGMSQTEPP-DF 105
Db 60 T-TGCSKMDNLTCTWPTTPRGQAVLDCLFLQFAPIHGYNLSRSTEGNSQLEPGPY 118
QY 106 VDAGYSDP-----EDESKITFYLKAIYTLGYSVLSMLATGSIILCLFRKLHCTRNVI 161
Db 119 HTACGLNDRASLDQEQQTKFYNTVTKTYTIGYSLASLLVAMAILSLFRKLHCTRNVI 178
QY 162 HNLFLSFLTRAIISLVKDDVLYSSSGTLHCPDQPSWVGCKLSLVFLQYICIMANFWLL 221
Db 179 HMLFNSFLTRATAVFIKQMALFNSGEIDHCSE---ASVGCKAAVVFQYICVMAFWLL 235
QY 222 VEGLYLHTLL-VAMLPRRRCFLAYLLIGWGLTFCIGAWTAARLYLEDTCGWDTHDSVP 280
Db 236 VEGLYLTLAVSFTSERXYFNGYILIGWVSVFTITVTVRIYFEDFGWDTHNSL 295
QY 281 WVIIRIPILISIVNFVLSIRILLQKLTSPDVGNDQSQYKRLAKSTLLILPLFGVH 340
Db 296 WIIKAPILLISLVNPLFICIRIIVQKLRPPDIGNDSFYSRLAKSTLLILPLFGIH 355
QY 341 YMVFAVFPISISKYQILFELCLGFSQGLVAVLVFLNSEQCELRKWR----- 391
Db 356 YMFAPFPNPAQVKNVVELVGSFGGFVAILYCLNGEVOAELRRKWRHLLQGVIG 415
QY 392 --SRCTPSPASRDYRVCGSFRNGSEGALQPHRGSAQSFLOTETSVI 438
Db 416 WSSKSHQPPGGSGNATCSTQVSM-----LTRVSPSARRSSSFQAEVSLV 459

RESULT 11

JC2194
vasoactive intestinal peptide receptor precursor - human
C:Species: Homo sapiens (man)
C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Nov-1999
C:Accession: JC2194; JN0604; PC2289; S38397
R:Couvineau, A.; Ruyter-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carrero, I.; Ogier-Denis, Biochem. Biophys. Res. Commun. 200, 769-776, 1994
A:Title: Human intestinal VIP receptor: cloning and functional expression of two cDNA
A:Reference number: JC2194; MUID:94235025; PMID:8179610
A:Accession: JC2194
A:Molecule type: mRNA
A:Residues: 1-460 <COU>
A:Cross-references: EMBL:X75299; NID:G407461; PIDN:CAA53046.1; PID:G407462
A:Experimental source: jejunal epithelial cell; clone HIVR8
R:Sreedharan, S.P.; Patel, D.R.; Huang, J.X.; Goetzl, E.J.
Biochem. Biophys. Res. Commun. 193, 546-553, 1993
A:Title: Cloning and functional expression of a human neuroendocrine vasoactive intestinal peptide receptor
A:Reference number: JN0604; MUID:93290641; PMID:8390245
A:Accession: JN0604
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-284,288-460 <SRE>
A:Cross-references: GB:L13286; NID:G292903; PIDN:AAA36805.1; PID:G292904
R:Couvineau, A.; Gaudin, P.; Maoret, J.J.; Ruyter-Fessard, C.; Nicole, P.; Laburthe, M. Biochem. Biophys. Res. Commun. 206, 246-252, 1995
A:Title: Highly conserved aspartate 68, tryptophane 73 and glycine 109 in the N-termina
A:Reference number: PC2289; MUID:95118345; PMID:7818527
A:Accession: PC2289
A:Molecule type: mRNA
A:Residues: 63-129 <CO2>
C:Genetics:
A:Gene: GDB:VIPR1; RCD1; HVR1
A:Cross-references: GDB:128589; OMIM:192321
A:Map position: 3p22-3p22
C:Superfamily: glucagon receptor
C:Keywords: glycoprotein; hormone receptor; intestine; phosphoprotein; transmembrane pr
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-460/Product: vasoactive intestinal peptide receptor #status predicted <MAT>
F:145-168/Domain: transmembrane #status predicted <TM1>
F:176-194/Domain: transmembrane #status predicted <TM2>
F:216-234/Domain: transmembrane #status predicted <TM3>
F:255-277/Domain: transmembrane #status predicted <TM4>
F:299-319/Domain: transmembrane #status predicted <TM5>
F:346-363/Domain: transmembrane #status predicted <TM6>
F:377-395/Domain: transmembrane #status predicted <TM7>
F:58,69,100,293/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:76/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted
F:250/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F:450/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
Query Match 43.7%; Score 1024; DB 2; Length 460;
Best Local Similarity 46.0%; Pred. No. 3.4e-77;
Matches 216; Conservative 68; Mismatches 144; Indels 42; Gaps 13;
QY 1 MRTLPP-PALLATC-----WLLAPVNS-----IHPCECFHLEIOBEETKCAELLSQTEK 48
Db 1 MRPPSPHVRWLCVLAGALAC-ALRPAGSOASPOHECYQLQIEFQRCQCLEBAQLENET 60
QY 49 HKACSGVNDNITCWRPANVGETVTPCPKFSNFYSKAG-NISKNCTSDGMSQTEPP-DFV 106
Db 61 -IGCSKMDNLTCTWPTTPRGQAVLDCLFLQFAPIHGYNLSRSTEGNSQLEPGPY 119
QY 107 DACGYSDPE---DESKITFYLKAIYTLGYSVLSMLATGSIILCLFRKLHCTRNVIHL 163
Db 120 IACGLDDKAASLDEQQTNTFYGSVTKTYTIGYSLATLLVATALLSLFRKLHCTRNVIHM 179
QY 164 NLFSLFILRAISLVKDDVLYSSSGTLHCPDQPSWVGCKLSLVFLQYICIMANFWLLVE 223
Db 180 HLFISFILRAAVFIKQMALFNSGESDQCE---GSVCKAAVVFQYICVMAFWLLVE 236
QY 224 GLYHLTL-VAMLPRRRCFLAYLLIGWGLTFCIGAWTAARLYLEDTCGWDTHDSV 279
Db 237 GLYTLTLLAVSFTSERXYFNGYILIGWVSVFTITVTVRIYFEDFGWDTHNSL 296

[illegible]

RESULT 12

C;Species: Homo sapiens (man)
 C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 24-Nov-1999
 C;Accession: J021195; S42087
 R;Couvigneau, A.; Rouyer-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carretero, I.; Ogier-Denis
 Biochem. Biophys. Res. Commun. 200, 769-776. 1994
 A;Title: Human intestinal VIP receptor: cloning and functional expression of two cDNA en
 A;Reference number: J021194; MUID:94235025; PMID:8179610
 A;Accession: J021195
 A;Molecule type: mRNA
 A;Residues: 1-495 <COU>
 A;Cross-references: EMBL:X77777; NID:g456352; PIDN:CAA54814.1; PID:g456353
 A;Experimental source: jejunal epithelial cell

Query Match	43.5%	Score 1018;	DB 2;	Length 495;
Best Local Similarity	47.3%	Pred. No. 1.1e-76;		
Matches 208;	Conservative	69;	Mismatches 133;	Indels 30;
				Gaps 10;

Qy	19	NSIHPECRFHLEIOBEETFKABLLRSQTEKHKACSGVWDNITCWRPANVGETVTVPCKV	78
Db	66	SSLOEEDYVQIMIEVQHKQCLEEAQLENET-IGCSKMDNLTCTPATPRGQVWLACPLI	124
Qy	79	FSNFYSKAG-NISKNCTSDGWSFTFP-DFVDACGYSDEP---DESKTFYILVKAIVTLG	133
Db	125	FKLFSSIQGRVNSRSCDEGTHLEPGYPPTACGLDDKAAISLDEQQTWFSYKVTGYTIG	184
Qy	134	YVSIMSLATSGIILCLPRKLHCTRNYYIHLNLFISFILRAISLVKDDVLVSSSGTLHCP	193
Db	185	YGLSIATLLVATATLSILPRKLHCTRNYYIHMHLFISFILRAAAVFKDIALPDSGESDQS	244
Qy	194	DQPSWGCKLSLVFLOYCIWANFPWLAVEGLYLHTLL-VAMLPPRCFLAYLITGWLCP	252
Db	245	E---GSVGCKAAWFFQYCVANFPWLAVEGLYLYLLAAVFFSFRKTFWGLILGWGVP	301
Qy	253	TVICIGAWTAARLYLEDTG---CWTDNRHSVPWWIRIPILSIIYVNFVLFISIRILLQK	309
Db	302	STFTMWVTAIRIHEDYGLLRCDWTINGSL-WWIKGRLTSILVNFILFICIRILLQK	360

```

310 LTSPPDVGNDQSQYKRLAKSTLLLLPLFGVHVMVFAVFPISSSKYQILFELCLGSFQGL 369
    ||: | : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
361 LRPDDIRKSDSSPYSLRASTLLLLPLFGVHYIMEAFFPDNFKPKVMFELVGSFQGF 420
    ||: | : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
370 VVAVLYCFLNSEVQCELKKRW-----SRCPTPSASRDVRYVCGSSFSFRNGSEGA 418
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
421 VVAILYCFLNSEVQAEELRRKKRRWHLLQGVLGWNPXYRHPSGGSNGATCTQVSM----L 475
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
419 LQFHRSRAQSFLQTETSVI 438
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
476 TRVSPGARSSSFQAEVSLV 495
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

```

RESULT 13

secretin receptor - rat
S16319
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S16319
R;Ishihara, T.; Nakamura, S.; Kaziro, Y.; Takahashi, T.; Takahashi, K.; Nagata, S.
EMBO J. 10, 1635-1641, 1991
A:Title: Molecular cloning and expression of a cDNA encoding the secretin receptor.
A:Reference number: S16319, MUID:91266890; PMID:1646711
A:Accession: S16319
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-449 <ISH>
A:Cross-references: EMBL:X59132; NID:G57228; PIDN:CAA41849.1; PID:G57229
C:Superfamily: Glucagon receptor
C:Keywords: G protein-coupled receptor; transmembrane protein

```

Qy 1 MRTLPPALLITCWLl---APVNSIHPE-CRHFLEIQBEETKCAELLRSQ-----TEKHK 50
Db 5 MRPLRSLLLRLLLTAKAHTVGVPPRLCDVRRVILBEERAHCLQOLSGEKKKGALGPETAS 64
Qy 51 ACGSVWDNITCWRPNVGETVTPCPKVFNSFYSKAGNISKNCTSDGWSFEPDFVDACG 110
Db 65 GEGELWDNMSCWPPSAPARTVEVQCPKFLMLSNKNSGLFRNCIQDQWSETFPPDPIACG 124
Qy 111 --YSDEDESKITFYILKVAITYLGYSVLSMLATGSIILCFRKLHCTRNYIHLNIFLS 168
Db 125 VNINNSFNERRHAYLLKLKVMYTVGYSSSLAMLLVALSILCSFRHLRCHTRNYIHMHLFVS 184
Qy 169 FILRAISVLAKDDVLYSSGTLHCPDQSSWVGCKLSLVLOYCIEMANFWKLLVEGGLYTH 228
Db 185 FILRAUSNFIKDAVLFPSSDDVTVC---DAHVGQCKLVMIFFQYCIEMANYAWLLVEGGLYTH 241
Qy 229 TLL-VAMLPRRRCFLAYLLIGLGLPTVCIGAWTAARLYLEDTCWDNDHDSVPMWVIRIP 287
Db 242 TLLAISFFSERKYLQAFVLGLGWGSPAIFVALWAIWTRHFLENTGCWDNANASVWVWIRGP 301
Qy 288 ILLISIVNFVLISIRILLQKLSPDVCGNDQSQYKRLAKSTLIIILPLFGVHYWVPVAF 347
Db 302 VILSILINFIFFINILIRIMRKLRTQETRGSETNHYKRLAKSTLIIILPLFGIHYIYFAFS 361
Qy 348 P-SISCKYQILFELCLGSGFQGLVAVLYCFILNSEVQCELKRKWR---SRCPTSPASRDY 403
Db 362 P-EDAMEVOLFELALSGSFGGLVAVLYCFLNGEVOLEVKWQWOWHQBEPFLPVA--- 417
Qy 404 RVCGSFSRNGSEGALQFHRRSGRAQSPLOTETSVI 438
Db 418 --FNNFSF-NATNGPTHSTKASTEOSRIPRASII 449

```

RESULT 14

secretin receptor - human
JC2532
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence revision 11-Apr-1997 #text change 05-Nov-1999

C;Accession: JC2532
 R;Jiang, S.; Ulrich, C.
 Biochem. Biophys. Res. Commun. 207, 893-890, 1995
 A;Title: Molecular cloning and functional expression of a human pancreatic secretin receptor
 A;Reference number: JC2532; MUID:95169147; PMID:7864894
 A;Accession: JC2532
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-440 <JIA>
 A;Cross-references: EMBL:U20178; NID:9662795; PIDN:AACS0106.1; PID:9662796
 A;Experimental source: pancreas
 C;Genetics
 A;Gene: ~~GSR~~:SCTR
 A;Cross-references: GDB:270546; OMIM:182098
 A;Map position: 2q14.1-2q14.1
 C;Superfamily: glucagon receptor

Query Match 42.4%; Score 992.5; DB 2; Length 440;
 Best Local Similarity 47.9%; Pred. No. 1.3e-74;
 Matches 192; Conservative 72; Mismatches 122; Indels 15; Gaps 7;

Qy 1 MRTLPPALLICWLLAPVNSIHPCRFHELEIQEBETKC-AELLRSOT-----EKHKACS 53
 Db 9 LQQLLLPVLLAC-AAHSTGALPRLCDVLQVLWEEQDCLQELSREQTGDLTGEQFPVPGCE 67

Qy 54 GVNDNITCWRPANVGETVTVPCKVFSNFKAGNISKNTSDGWSETF--PDFVDACGY 111
 Db 68 GWNINISCPSSVPGRMVECEPRFLMLTBSNGSLFRNCTQDQGWSETFPRPNLACAVN 127

Qy 112 SDPEDESKITFYILVKALTYLGYSVLSMLATGSIILCLFRKLHCTRYIHNLFLSFL 171
 Db 128 NDSSNEKRHSYLLKVMYTVGYSSSLVALLVALGILCAFRRLHCTRYIHMLFVSPIL 187

Qy 172 PAISVLVQDDVLYSSSTGLHCPDQSPSSWGCKLSLVFLQYICIMANFFWLYEGLYLHLL 231
 Db 188 RALSNFIDKAVLFSGDDVTYC---DAHRAGCKLVMVLFQYICIMANYSWLLVEGLYLHLL 244

Qy 232 -VAMLPFRRCFLAYLLIGWGLPTVCIGAWTARLYLEDTGWDNDHSVPWWVIRIPILI 290
 Db 245 AISPFSEKYLQGFVAFGWSGPAIFVALWATARHLEDVGCWDINANASIWWIRGPFIL 304

Qy 291 SIIVNVLFIPIIRILLQKLSPDVGGNDQSQYKRLAKSTLLPLFGVHYMVFAVFPIS 350
 Db 305 SILINFIILIRILIRILKRLTQETRGNEVSHYKRLARSTLLILPLFGIHVIFAFSP-E 363

Qy 351 ISSKYQILFELCLGSGFQGLVAVLYCFLNSENVCQELKRW 391
 Db 364 DAMEIQLFELALASFGLLVAVLYCFLNGEVQLEVQKRW 404

RESULT 15
 S33449
 pituitary adenylate cyclase-activating polypeptide receptor homolog - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
 C;Accession: S33449
 R;Svoboda, M.; Ciccarelli, E.; Tasteno, M.; Christophe, J.
 submitted to the EMBL Data Library, May 1993
 A;Description: Molecular cloning of a PACAP-type receptor.
 A;Reference number: S33449
 A;Accession: S33449
 A;Status: Preliminary
 A;Molecule type: mRNA
 A;Residues: 1-381 <SVO>
 A;Cross-references: EMBL:Z22735; NID:9311228; PIDN:CAA80429.1; PID:9311229
 C;Superfamily: glucagon receptor

Query Match 42.3%; Score 991; DB 2; Length 381;
 Best Local Similarity 51.1%; Pred. No. 1.5e-74;
 Matches 192; Conservative 53; Mismatches 97; Indels 34; Gaps 4;

Qy 91 KNCISDGHSETFPDFVACGYSD--PEDESKITFYILVKALTYLGYSVLSMLATGSIIL 148

Db 1 RNCIEDGWSSEFFPHYFDACGDDYEPESGDQDYLYLSVRALYTVGYSTSLATLTAMVIL 60
 Qy 149 CLFRKLHCTRYIHNLFLSFLIRALISVLVKDDVLYSSSTGLHCPDQSPSSWGCKLSLVF 208
 Db 61 CRFRKLHCTRYIHNLFLSFLIRALISVFIKDWILYAEQDSSHC---FVSTVECKAVAVF 117
 Qy 209 LQYICIMANFFWLYEGLYLHLLV-AMLPFRRCFLAYLLIGWGLPTVCIGAWTARLYLE 267
 Db 118 FHYCVSNYFWLFEGLYLFLLVETFFERRFYWTIIIGWGLPTVCVTWAVRLYFD 177
 Qy 268 DTGWDNDHSVPWWVIRIPILISIIYVFLFISIIIRILLQKLSPTDVGGNDQSQY--- 323
 Db 178 DAGCWDNDSTALWVWIKGPVWGSIMVNFVFIGIILVQKLSQSPDMGNESSIYFSCV 237
 Qy 324 -----KRLAKSTLLILPLFGVHYMVFAVFPISISSKYQILF 359
 Db 238 QKCYCKPQRAQHSCKMSLSLTITRLARSTLLILPLFGIHVITVFAFSPENVSKRLV 297
 Qy 360 ELCLGSGFQGLVAVLYCFLNSENVCQELKRWRSRCPSPASRDYRVCGSGSFRNGSEAL 419
 Db 298 ELGLGSGFQGVAVLYCFLNGEVQAEIKRWRSWKVNRYPMTDFKRRHPSLASSGVNGGT 357
 Qy 420 QFHRGSAQSFLOTET 435
 Db 358 QLSILSKSSSHVRMST 373

Search completed: June 22, 2004, 08:59:33
 Job time : 21 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 22, 2004, 08:57:39 ; Search time 183 Seconds
(without alignments)
2336.128 Million cell updates/sec

Title: US-09-983-000A-20

Perfect score: 2342

Sequence: 1 MRTLPLPALLTCWLLAPVNS.....LQFGRSRAQSFLQTETSVI 438

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA Main:*

- 1: /cgn2_6/ptodata/2/paa/PCTUS COMB.pcp.*
- 2: /cgn2_6/ptodata/2/paa/US06 COMB.pcp.*
- 3: /cgn2_6/ptodata/2/paa/US07 COMB.pcp.*
- 4: /cgn2_6/ptodata/2/paa/US08 COMB.pcp.*
- 5: /cgn2_6/ptodata/2/paa/US08 COMB.pcp.*
- 6: /cgn2_6/ptodata/2/paa/US08 COMB.pcp.*
- 7: /cgn2_6/ptodata/2/paa/US08 COMB.pcp.*
- 8: /cgn2_6/ptodata/2/paa/US08 COMB.pcp.*
- 9: /cgn2_6/ptodata/2/paa/US08 COMB.pcp.*
- 10: /cgn2_6/ptodata/2/paa/US08 COMB.pcp.*
- 11: /cgn2_6/ptodata/2/paa/US08 COMB.pcp.*
- 12: /cgn2_6/ptodata/2/paa/US08 COMB.pcp.*
- 13: /cgn2_6/ptodata/2/paa/US08 COMB.pcp.*
- 14: /cgn2_6/ptodata/2/paa/US09 COMB.pcp.*
- 15: /cgn2_6/ptodata/2/paa/US09 COMB.pcp.*
- 16: /cgn2_6/ptodata/2/paa/US09 COMB.pcp.*
- 17: /cgn2_6/ptodata/2/paa/US09 COMB.pcp.*
- 18: /cgn2_6/ptodata/2/paa/US09 COMB.pcp.*
- 19: /cgn2_6/ptodata/2/paa/US09 COMB.pcp.*
- 20: /cgn2_6/ptodata/2/paa/US09 COMB.pcp.*
- 21: /cgn2_6/ptodata/2/paa/US09 COMB.pcp.*
- 22: /cgn2_6/ptodata/2/paa/US09 COMB.pcp.*
- 23: /cgn2_6/ptodata/2/paa/US09 COMB.pcp.*
- 24: /cgn2_6/ptodata/2/paa/US09 COMB.pcp.*
- 25: /cgn2_6/ptodata/2/paa/US09 COMB.pcp.*
- 26: /cgn2_6/ptodata/2/paa/US09 COMB.pcp.*
- 27: /cgn2_6/ptodata/2/paa/US10 COMB.pcp.*
- 28: /cgn2_6/ptodata/2/paa/US10 COMB.pcp.*
- 29: /cgn2_6/ptodata/2/paa/US10 COMB.pcp.*
- 30: /cgn2_6/ptodata/2/paa/US10 COMB.pcp.*
- 31: /cgn2_6/ptodata/2/paa/US10 COMB.pcp.*
- 32: /cgn2_6/ptodata/2/paa/US10 COMB.pcp.*
- 33: /cgn2_6/ptodata/2/paa/US60 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1	2342	100.0	438	1	PCT-US00-21278-24	Sequence 24, Appl
2	2342	100.0	438	1	PCT-US01-08656-8498	Sequence 8498, Ap
3	2342	100.0	438	20	US-03-631-603-24	Sequence 24, Appl
4	2342	100.0	438	20	US-09-694-519-10	Sequence 10, Appl
5	2342	100.0	438	25	US-09-983-000A-20	Sequence 20, Appl
6	2342	100.0	438	28	US-10-273-573-8498	Sequence 8498, Ap
7	2342	100.0	438	30	US-10-404-618-90	Sequence 90, Appl
8	2342	100.0	438	31	US-10-652-981-20	Sequence 20, Appl
9	2342	100.0	438	33	US-60-443-566-4403	Sequence 4403, Ap
10	2342	100.0	438	33	US-60-453-050-10294	Sequence 10294, A
11	2342	100.0	438	33	US-60-453-135-10294	Sequence 10294, A
12	2342	100.0	438	33	US-60-455-444-5513	Sequence 5513, Ap
13	2342	100.0	438	33	US-60-465-241-5513	Sequence 5513, Ap
14	2342	100.0	438	33	US-60-466-412-10294	Sequence 10294, A
15	2342	100.0	438	33	US-60-500-315-1460	Sequence 1460, Ap
16	2342	100.0	438	33	US-60-500-315-1461	Sequence 1461, Ap
17	2342	100.0	492	24	US-09-949-004-465	Sequence 465, App
18	2342	100.0	500	1	PCT-US01-14827-11843	Sequence 11843, A
19	2331	99.5	438	9	US-08-538-816-1	Sequence 1, Appli
20	2331	99.5	438	20	US-09-694-519-12	Sequence 12, Appl
21	2331	99.5	454	1	PCT-US01-08631-58175	Sequence 58175, A
22	2327	99.4	438	20	US-03-694-519-11	Sequence 11, Appl
23	2327	99.4	438	21	US-09-708-344-19	Sequence 19, Appl
24	2327	99.4	438	21	US-09-708-344A-19	Sequence 19, Appl
25	2327	99.4	438	21	US-09-708-365-19	Sequence 19, Appl
26	2327	99.4	438	21	US-09-708-392-19	Sequence 19, Appl
27	2327	99.4	438	21	US-09-708-393-19	Sequence 19, Appl
28	2327	99.4	438	21	US-09-708-393A-19	Sequence 19, Appl
29	2327	99.4	438	27	US-10-157-031-237	Sequence 237, App
30	2327	99.4	438	28	US-10-225-567A-471	Sequence 471, App
31	2327	99.4	438	31	US-10-686-282-19	Sequence 19, Appl
32	2327	99.4	438	31	US-10-686-349-19	Sequence 19, Appl
33	2327	99.4	438	31	US-10-686-390-19	Sequence 19, Appl
34	2321	98.1	438	23	US-03-826-509-581	Sequence 581, App
35	2294	98.0	484	33	US-60-245-228-327	Sequence 327, App
36	2294	98.0	484	33	US-60-258-272-129	Sequence 129, App
37	2245.5	95.9	437	8	US-08-437-466-1	Sequence 1, Appli
38	2239.5	95.6	431	9	US-08-538-816-9	Sequence 9, Appli
39	2049	87.5	517	1	PCT-US03-28227-3445	Sequence 3445, Ap
40	2045	87.3	452	21	US-09-724-676-82337	Sequence 82337, A
41	2045	87.3	452	21	US-09-724-676A-82337	Sequence 82337, A
42	2045	87.3	452	27	US-10-130-138A-133	Sequence 133, App
43	2045	87.3	455	21	US-09-724-676-82335	Sequence 82335, A
44	2045	87.3	455	21	US-09-724-676-82336	Sequence 82336, A
45	2045	87.3	455	21	US-09-724-676A-82335	Sequence 82335, A

ALIGNMENTS

RESULT 1

PCT-US00-21278-24

Sequence 24, Application PC/TUS0021278

GENERAL INFORMATION:

APPLICANT: Hodge, Martin R.

APPLICANT: Lloyd, Clare

APPLICANT: Weich, Nadine

TITLE OF INVENTION: 15571, A Novel GPCR-like Molecule of the Secretin-Like Family and Uses Thereof

FILE REFERENCE: 5800-48A

CURRENT APPLICATION NUMBER: PCT/US00/21278

CURRENT FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: 09/515,781

PRIOR FILING DATE: 2000-02-29

PRIOR APPLICATION NUMBER: 60/146,916

PRIOR FILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 24

LENGTH: 438

TYPE: PRT

ORGANISM: Homo sapiens

PCT-US00-21278-24

Query Match 100.0%; Score 2342; DB 1; Length 438;
Best Local Similarity 100.0%; Pred. No. 1e-212;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPCRHLEIQBEETKCAELLRSQTEKHKACSGVNDIT 60
DB 1 MRTLPPALLTCWLLAPVNSIHPCRHLEIQBEETKCAELLRSQTEKHKACSGVNDIT 60

QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGSETFPDFVACGYSDPEDESKI 120
DB 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGSETFPDFVACGYSDPEDESKI 120

QY 121 TFYILVKAIVTLGYSVSLMSLATGSIILCLFRKLHCTRNIIHLNLFILRAISVLVKD 180
DB 121 TFYILVKAIVTLGYSVSLMSLATGSIILCLFRKLHCTRNIIHLNLFILRAISVLVKD 180

QY 181 DVLYSSGTLHCPDPQSSWGCKLSLVFLQYCI MANFFWLLVEGLYHLTHLVA MLPPRR 240
DB 181 DVLYSSGTLHCPDPQSSWGCKLSLVFLQYCI MANFFWLLVEGLYHLTHLVA MLPPRR 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSDVPWWIRIPILISIIIVNVLFI 300
DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSDVPWWIRIPILISIIIVNVLFI 300

QY 301 SIIRILLOKLTSPDVGGNDQSOYKRLAKSTLLIPLFGVHYVMFAVPISSISKYQILFE 360
DB 301 SIIRILLOKLTSPDVGGNDQSOYKRLAKSTLLIPLFGVHYVMFAVPISSISKYQILFE 360

QY 361 LCLGSFQGLVAVLYCFNLSEVOCELKRWKRCPTPSASRDYRVCGSSFRNGSEGAQ 420
DB 361 LCLGSFQGLVAVLYCFNLSEVOCELKRWKRCPTPSASRDYRVCGSSFRNGSEGAQ 420

QY 421 FHRGSAQSFLQTETSVI 438
DB 421 FHRGSAQSFLQTETSVI 438

RESULT 2
PCT-US01-08656-8498
; Sequence 8498, Application PC/TUS0108656
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: PCT/US01/08656
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-16
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 8498
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (133)..(179)
; OTHER INFORMATION: G-protein coupled receptors family 2 proteins domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00649B, p-value=9.625e-
; OTHER INFORMATION: 38, raw score of 20.68
; NAME/KEY: DOMAIN
; LOCATION: (123)..(382)
; OTHER INFORMATION: 7 transmembrane receptor (Secretin family) domain identified
; OTHER INFORMATION: by Pfam, accession name 7tm_2, E-value=8.8e-131, Pfam score of
; OTHER INFORMATION: 447.9
PCT-US01-08656-8498

Query Match 100.0%; Score 2342; DB 1; Length 438;
Best Local Similarity 100.0%; Pred. No. 1e-212;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPCRHLEIQBEETKCAELLRSQTEKHKACSGVNDIT 60
DB 1 MRTLPPALLTCWLLAPVNSIHPCRHLEIQBEETKCAELLRSQTEKHKACSGVNDIT 60

QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGSETFPDFVACGYSDPEDESKI 120
DB 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGSETFPDFVACGYSDPEDESKI 120

QY 121 TFYILVKAIVTLGYSVSLMSLATGSIILCLFRKLHCTRNIIHLNLFILRAISVLVKD 180
DB 121 TFYILVKAIVTLGYSVSLMSLATGSIILCLFRKLHCTRNIIHLNLFILRAISVLVKD 180

QY 181 DVLYSSGTLHCPDPQSSWGCKLSLVFLQYCI MANFFWLLVEGLYHLTHLVA MLPPRR 240
DB 181 DVLYSSGTLHCPDPQSSWGCKLSLVFLQYCI MANFFWLLVEGLYHLTHLVA MLPPRR 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSDVPWWIRIPILISIIIVNVLFI 300
DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSDVPWWIRIPILISIIIVNVLFI 300

QY 301 SIIRILLOKLTSPDVGGNDQSOYKRLAKSTLLIPLFGVHYVMFAVPISSISKYQILFE 360
DB 301 SIIRILLOKLTSPDVGGNDQSOYKRLAKSTLLIPLFGVHYVMFAVPISSISKYQILFE 360

QY 361 LCLGSFQGLVAVLYCFNLSEVOCELKRWKRCPTPSASRDYRVCGSSFRNGSEGAQ 420
DB 361 LCLGSFQGLVAVLYCFNLSEVOCELKRWKRCPTPSASRDYRVCGSSFRNGSEGAQ 420

QY 421 FHRGSAQSFLQTETSVI 438
DB 421 FHRGSAQSFLQTETSVI 438

RESULT 3
US-09-631-603-24
; Sequence 24, Application US/09631603
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Lloyd, Clare
; APPLICANT: Weich, Nadine
; TITLE OF INVENTION: 15571, A Novel GPCR-like Molecule of the
; FILE REFERENCE: Secretin-Like Family and Uses Thereof
; CURRENT APPLICATION NUMBER: US/09/631,603
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/515,781
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/146,916
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-631-603-24

Query Match 100.0%; Score 2342; DB 20; Length 438;
Best Local Similarity 100.0%; Pred. No. 1e-212;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPCRHLEIQBEETKCAELLRSQTEKHKACSGVNDIT 60
DB 1 MRTLPPALLTCWLLAPVNSIHPCRHLEIQBEETKCAELLRSQTEKHKACSGVNDIT 60

QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGSETFPDFVACGYSDPEDESKI 120
DB 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGSETFPDFVACGYSDPEDESKI 120

QY 121 TFYILVKAIVTLGYSVSLMSLATGSIILCLFRKLHCTRNIIHLNLFILRAISVLVKD 180
DB 121 TFYILVKAIVTLGYSVSLMSLATGSIILCLFRKLHCTRNIIHLNLFILRAISVLVKD 180

```
QY 181 DVLSSGTLHCPDOPSSWVGKLSLVFLQYCI MANFWLLVEGLYHLTLVAMLPBRC 240
Db 181 DVLSSGTLHCPDOPSSWVGKLSLVFLQYCI MANFWLLVEGLYHLTLVAMLPBRC 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPWVIRIPILISIIIVNFVLI 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPWVIRIPILISIIIVNFVLI 300
QY 301 SIIRILLQKLTSPDVGNDQSKYKLAKTLLIPLFGVHYMVFAVFPISISKYQILFE 360
Db 301 SIIRILLQKLTSPDVGNDQSKYKLAKTLLIPLFGVHYMVFAVFPISISKYQILFE 360
QY 361 LCLGSFQGLVAVLYCFNLSEVQCELRKWRRCPTPSASRDYRVCGSFSRNGSEGALQ 420
Db 361 LCLGSFQGLVAVLYCFNLSEVQCELRKWRRCPTPSASRDYRVCGSFSRNGSEGALQ 420
QY 421 FHRGSAQSFLOTETSVI 438
Db 421 FHRGSAQSFLOTETSVI 438

RESULT 4
US-09-694-519-10
; Sequence 10, Application US/09694519
; GENERAL INFORMATION:
; APPLICANT: Isfort, Robert
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or
; FILE REFERENCE: 8311
; CURRENT APPLICATION NUMBER: US/09/694,519
; CURRENT FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 438
; TYPE: PRT
; ORGANISM: homo sapiens;
US-09-694-519-10
```

```
Query Match 100.0%; Score 2342; DB 20; Length 438;
Best Local Similarity 100.0%; Pred. No. 1e-212;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHLEIQEETKCAELRSQTEKHKACSGVWDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPECRFHLEIQEETKCAELRSQTEKHKACSGVWDNIT 60
QY 61 CWRPANVGETVTPCPKVFNFYSKAGNISKNCTSDGWSSETFPDFVACGYSDPDESKI 120
Db 61 CWRPANVGETVTPCPKVFNFYSKAGNISKNCTSDGWSSETFPDFVACGYSDPDESKI 120
QY 121 TFYIIVKAIYTLGYSVLSLMTAGSIILCLPKLHCTRYIHLNPLSFILRAISVLVKD 180
Db 121 TFYIIVKAIYTLGYSVLSLMTAGSIILCLPKLHCTRYIHLNPLSFILRAISVLVKD 180
QY 181 DVLSSGTLHCPDOPSSWVGKLSLVFLQYCI MANFWLLVEGLYHLTLVAMLPBRC 240
Db 181 DVLSSGTLHCPDOPSSWVGKLSLVFLQYCI MANFWLLVEGLYHLTLVAMLPBRC 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPWVIRIPILISIIIVNFVLI 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPWVIRIPILISIIIVNFVLI 300
QY 301 SIIRILLQKLTSPDVGNDQSKYKLAKTLLIPLFGVHYMVFAVFPISISKYQILFE 360
Db 301 SIIRILLQKLTSPDVGNDQSKYKLAKTLLIPLFGVHYMVFAVFPISISKYQILFE 360
QY 361 LCLGSFQGLVAVLYCFNLSEVQCELRKWRRCPTPSASRDYRVCGSFSRNGSEGALQ 420
Db 361 LCLGSFQGLVAVLYCFNLSEVQCELRKWRRCPTPSASRDYRVCGSFSRNGSEGALQ 420
```

```
QY 421 FHRGSAQSFLOTETSVI 438
Db 421 FHRGSAQSFLOTETSVI 438

RESULT 5
US-09-983-000a-20
; Sequence 20, Application US/09983000A
; GENERAL INFORMATION:
; APPLICANT: Agy Therapeutics
; APPLICANT: Melcher, Thorsten
; APPLICANT: Mueller, Sabine
; APPLICANT: Chin, Daniel
; TITLE OF INVENTION: USE OF PROTEIN BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUALI
; FILE REFERENCE: 263/180 -- Peagleman -- AGY
; CURRENT APPLICATION NUMBER: US/09/983,000A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(23)
; OTHER INFORMATION: Potential
; NAME/KEY: GENE
; LOCATION: (1)..(438)
; OTHER INFORMATION: Vasoactive Intestinal Peptide Receptor 2
; NAME/KEY: CHAIN
; LOCATION: (24)..(438)
; OTHER INFORMATION: Vasoactive Intestinal Polypeptide Receptor 2
; NAME/KEY: DOMAIN
; LOCATION: (24)..(126)
; OTHER INFORMATION: 1 (Potential)
; NAME/KEY: TRANSMEM
; LOCATION: (127)..(151)
; OTHER INFORMATION: 1 (Potential)
; NAME/KEY: DOMAIN
; LOCATION: (152)..(158)
; OTHER INFORMATION: Cytoplasmic (potential)
; NAME/KEY: TRANSMEM
; LOCATION: (159)..(178)
; OTHER INFORMATION: 2 (Potential)
; NAME/KEY: DOMAIN
; LOCATION: (179)..(203)
; OTHER INFORMATION: Extracellular (Potential)
; NAME/KEY: TRANSMEM
; LOCATION: (204)..(227)
; OTHER INFORMATION: 3 (Potential)
; NAME/KEY: DOMAIN
; LOCATION: (228)..(240)
; OTHER INFORMATION: Cytoplasmic (Potential)
; NAME/KEY: TRANSMEM
; LOCATION: (241)..(262)
; OTHER INFORMATION: 4 (Potential)
; NAME/KEY: DOMAIN
; LOCATION: (263)..(279)
; OTHER INFORMATION: Extracellular (Potential)
; NAME/KEY: TRANSMEM
; LOCATION: (280)..(303)
; OTHER INFORMATION: 5 (Potential)
; NAME/KEY: DOMAIN
; LOCATION: (304)..(328)
; OTHER INFORMATION: Cytoplasmic (Potential)
; NAME/KEY: TRANSMEM
; LOCATION: (329)..(348)
; OTHER INFORMATION: 6 (Potential)
; NAME/KEY: DOMAIN
; LOCATION: (349)..(360)
; OTHER INFORMATION: Extracellular (Potential)
```

NAME/KEY: TRANSMEM
LOCATION: (361)..(380)
OTHER INFORMATION: 7 (Potential)
NAME/KEY: DOMAIN
LOCATION: (381)..(438)
OTHER INFORMATION: Cytoplasmic (potential)
NAME/KEY: CARBOHYD
LOCATION: (58)..(58)
OTHER INFORMATION: N-linked (GLCNAC...) (Potential)
NAME/KEY: CARBOHYD
LOCATION: (88)..(88)
OTHER INFORMATION: N-linked (GLCNAC...) (Potential)
NAME/KEY: CARBOHYD
LOCATION: (92)..(92)
OTHER INFORMATION: N-linked (GLCNAC...) (Potential)

US-09-983-000A-20

Query Match 100.0%; Score 2342; DB 25; Length 438;
Best Local Similarity 100.0%; Pred. No. 1e-212;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRPHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPECRPHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60
QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDFVDACGYSDPEDESKI 120
Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDFVDACGYSDPEDESKI 120
QY 121 TFYILVKAITYLGYSVLSMSLATGSIILCLPRKLHCTRNHYIHLNLFSLFILRAISVLVKD 180
Db 121 TFYILVKAITYLGYSVLSMSLATGSIILCLPRKLHCTRNHYIHLNLFSLFILRAISVLVKD 180
QY 181 DVLSSSGTLCPCDPQSSWVGCKLSLVFQYICIMANFVLLVEGLYHLLVAMLPERRC 240
Db 181 DVLSSSGTLCPCDPQSSWVGCKLSLVFQYICIMANFVLLVEGLYHLLVAMLPERRC 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIIIVNFVLF 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIIIVNFVLF 300
QY 301 SIIRILLQKLTSPDVGNDQSYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQILFE 360
Db 301 SIIRILLQKLTSPDVGNDQSYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQILFE 360
QY 361 LCLGSFQGLVAVLYCFINSEVQCELKRWKRSRCPGPSASRDYRVCGSSFRNGSEGLAQ 420
Db 361 LCLGSFQGLVAVLYCFINSEVQCELKRWKRSRCPGPSASRDYRVCGSSFRNGSEGLAQ 420
QY 421 FHRGSAQSFLQTETSVI 438
Db 421 FHRGSAQSFLQTETSVI 438

RESULT 6

US-10-273-573-8498
Sequence 8498, Application US/10273573
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: US/10/273, 573
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522, 929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770, 160
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
SOFTWARE: Custom
SEQ ID NO 8498
LENGTH: 438
TYPE: PRT
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: DOMAIN
LOCATION: (133)..(179)
OTHER INFORMATION: G-protein coupled receptors family 2 proteins domain
OTHER INFORMATION: identified by eMATRIX, accession number BL00649B, p-value=9.625e-
OTHER INFORMATION: 38, raw score of 20.68
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (123)..(382)
OTHER INFORMATION: 7 transmembrane receptor (Secretin family) domain identified
OTHER INFORMATION: by Pfam, accession name 7tm_2, E-value=8.8e-131, Pfam score of
OTHER INFORMATION: 447.9
US-10-273-573-8498

Query Match 100.0%; Score 2342; DB 28; Length 438;
Best Local Similarity 100.0%; Pred. No. 1e-212;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRPHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPECRPHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60
QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDFVDACGYSDPEDESKI 120
Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDFVDACGYSDPEDESKI 120
QY 121 TFYILVKAITYLGYSVLSMSLATGSIILCLPRKLHCTRNHYIHLNLFSLFILRAISVLVKD 180
Db 121 TFYILVKAITYLGYSVLSMSLATGSIILCLPRKLHCTRNHYIHLNLFSLFILRAISVLVKD 180
QY 181 DVLSSSGTLCPCDPQSSWVGCKLSLVFQYICIMANFVLLVEGLYHLLVAMLPERRC 240
Db 181 DVLSSSGTLCPCDPQSSWVGCKLSLVFQYICIMANFVLLVEGLYHLLVAMLPERRC 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIIIVNFVLF 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIIIVNFVLF 300
QY 301 SIIRILLQKLTSPDVGNDQSYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQILFE 360
Db 301 SIIRILLQKLTSPDVGNDQSYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQILFE 360
QY 361 LCLGSFQGLVAVLYCFINSEVQCELKRWKRSRCPGPSASRDYRVCGSSFRNGSEGLAQ 420
Db 361 LCLGSFQGLVAVLYCFINSEVQCELKRWKRSRCPGPSASRDYRVCGSSFRNGSEGLAQ 420
QY 421 FHRGSAQSFLQTETSVI 438
Db 421 FHRGSAQSFLQTETSVI 438

RESULT 7

US-10-404-618-90
Sequence 90, Application US/10404618
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
APPLICANT: Lloyd, Clare M.
APPLICANT: Weich, Nadine S.
APPLICANT: Lora, Jose M.
APPLICANT: White, David
APPLICANT: Glucksmann, Maria A.
APPLICANT: Robison, Keith E.
APPLICANT: Silos-Santiago, Immaculada
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: Curtis, Rory A.J.
TITLE OF INVENTION: NOVEL 15571, 2465, 14266, 2882, 52871,
TITLE OF INVENTION: 8203 AND 16852 MOLECULES AND USES THEREFOR
FILE REFERENCE: MPI03-0530MNM
CURRENT APPLICATION NUMBER: US/10/404, 618
CURRENT FILING DATE: 2003-04-01
PRIOR APPLICATION NUMBER: 09/631, 603
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/515, 781

```

; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/146,916
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 09/794,763
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/185,942
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/634,392
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 09/176,075
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/013,634
; PRIOR FILING DATE: 1998-01-26
; PRIOR APPLICATION NUMBER: 09/884,430
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/269,758
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-404-618-90

Query Match      100.0%; Score 2342; DB 30; Length 438;
Best Local Similarity 100.0%; Pred. No. 1e-212;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPCKRFLHLEIOEETKCAELLRSQTEKHKACSGVWDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPCKRFLHLEIOEETKCAELLRSQTEKHKACSGVWDNIT 60

QY 61 CWRPANVGTTVPCPKVSNFYKAGNISKNTSDGWSCTPDVDAAGYSDPEDESKI 120
Db 61 CWRPANVGTTVPCPKVSNFYKAGNISKNTSDGWSCTPDVDAAGYSDPEDESKI 120

QY 121 TFVILVKALYTLGYSVLSLMTAGSIILCLFRKLHCTRNVIHNLFLSFLRAISVLVD 180
Db 121 TFVILVKALYTLGYSVLSLMTAGSIILCLFRKLHCTRNVIHNLFLSFLRAISVLVD 180

QY 181 DVLYSSGTLHCPDQPSWVGCKLSVFLQYCIIMANFFMLLVEGLYLHTLLVAMLPFRC 240
Db 181 DVLYSSGTLHCPDQPSWVGCKLSVFLQYCIIMANFFMLLVEGLYLHTLLVAMLPFRC 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIIIVNFVLT 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIIIVNFVLT 300

QY 301 SIIRILLOKLTSPDVGNQDSQYKRLAKSTLLILPLFGVHYMVFAVFPISISSKYQILPE 360
Db 301 SIIRILLOKLTSPDVGNQDSQYKRLAKSTLLILPLFGVHYMVFAVFPISISSKYQILPE 360

QY 361 LCLGSFQGLVAVLYLFLNSEVOCELKRWRSRCPPTPSASRDYRVCGSSFSRNGSEGAQ 420
Db 361 LCLGSFQGLVAVLYLFLNSEVOCELKRWRSRCPPTPSASRDYRVCGSSFSRNGSEGAQ 420

QY 421 FHRGSAQSFLOTETSVI 438
Db 421 FHRGSAQSFLOTETSVI 438

RESULT 8
US-10-652-981-20
; Sequence 20, Application US/10652981
; GENERAL INFORMATION:
; APPLICANT: AGY Therapeutics
; APPLICANT: Melcher, Thorsten
; APPLICANT: Mueller, Sabine
; APPLICANT: Chien, Daniel
; TITLE OF INVENTION: USE OF PROTEIN BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUALIZ
; TITLE OF INVENTION: OF BRAIN TUMORS
```

```

; FILE REFERENCE: 263/180 -- PBagleman -- AGY
; CURRENT APPLICATION NUMBER: US/10/652,981
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US/09/983,000A
; PRIOR FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(23)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: GENE
; LOCATION: (1)..(438)
; OTHER INFORMATION: Vasoactive Intestinal Peptide Receptor 2
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (24)..(438)
; OTHER INFORMATION: Vasoactive Intestinal Polypeptide Receptor 2
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (24)..(126)
; OTHER INFORMATION: 1 (Potential)
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (127)..(151)
; OTHER INFORMATION: 1 (Potential)
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (152)..(158)
; OTHER INFORMATION: Cytoplasmic (potential)
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (159)..(178)
; OTHER INFORMATION: 2 (Potential)
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (179)..(203)
; OTHER INFORMATION: Extracellular (Potential)
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (204)..(227)
; OTHER INFORMATION: 3 (Potential)
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (228)..(240)
; OTHER INFORMATION: Cytoplasmic (Potential)
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (241)..(262)
; OTHER INFORMATION: 4 (Potential)
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (263)..(279)
; OTHER INFORMATION: Extracellular (Potential)
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (280)..(303)
; OTHER INFORMATION: 5 (Potential)
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (304)..(328)
; OTHER INFORMATION: Cytoplasmic (Potential)
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (329)..(348)
; OTHER INFORMATION: 6 (Potential)
; FEATURE:
; NAME/KEY: DOMAIN
```



```
; LOCATION: (349)..(360)
; OTHER INFORMATION: Extracellular (Potential)
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (361)..(380)
; OTHER INFORMATION: 7 (Potential)
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (381)..(438)
; OTHER INFORMATION: Cytoplasmic (potential)
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (58)..(58)
; OTHER INFORMATION: N-linked (GLCNAC...) (Potential)
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (88)..(88)
; OTHER INFORMATION: N-linked (GLCNAC...) (Potential)
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (92)..(92)
; OTHER INFORMATION: N-linked (GLCNAC...) (Potential)
; US-10-652-981-20

Query Match      100.0%; Score 2342; DB 31; Length 438;
Best Local Similarity 100.0%; Pred. No. 1e-212;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60

Qy 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDVPDAGYSDPEDESKI 120
Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDVPDAGYSDPEDESKI 120

Qy 121 TFYILVKAIYTLGYSVLSMSLATGSIILCLFRKLHCTRNHYIHLNLFILRAISVLVKD 180
Db 121 TFYILVKAIYTLGYSVLSMSLATGSIILCLFRKLHCTRNHYIHLNLFILRAISVLVKD 180

Qy 181 DVLYSSGTLHCPDQPSWVGCKSLVFLQVCIMANFFWLLVEGLYLHTLLVAMLPERRC 240
Db 181 DVLYSSGTLHCPDQPSWVGCKSLVFLQVCIMANFFWLLVEGLYLHTLLVAMLPERRC 240

Qy 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIIIVNFVLF 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIIIVNFVLF 300

Qy 301 SIIRILLQKLTSPDVGNDQSOYKRLAKSTLLIPLFGVHYWVFAVPFISISKYQILFE 360
Db 301 SIIRILLQKLTSPDVGNDQSOYKRLAKSTLLIPLFGVHYWVFAVPFISISKYQILFE 360

Qy 361 LCLGSFQGLVVAVLYCFNLSEVQCELKRWKRSRCPGPSASRDYRVCGSSFRNGSEGAQ 420
Db 361 LCLGSFQGLVVAVLYCFNLSEVQCELKRWKRSRCPGPSASRDYRVCGSSFRNGSEGAQ 420

Qy 421 FHRGSRAGSFLQTETSVI 438
Db 421 FHRGSRAGSFLQTETSVI 438

RESULT 9
US-60-443-566-4403
; Sequence 4403, Application US/60443566
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001447
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 25102
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4403
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-443-566-4403

Query Match      100.0%; Score 2342; DB 33; Length 438;
Best Local Similarity 100.0%; Pred. No. 1e-212;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60

Qy 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDVPDAGYSDPEDESKI 120
Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDVPDAGYSDPEDESKI 120

Qy 121 TFYILVKAIYTLGYSVLSMSLATGSIILCLFRKLHCTRNHYIHLNLFILRAISVLVKD 180
Db 121 TFYILVKAIYTLGYSVLSMSLATGSIILCLFRKLHCTRNHYIHLNLFILRAISVLVKD 180

Qy 181 DVLYSSGTLHCPDQPSWVGCKSLVFLQVCIMANFFWLLVEGLYLHTLLVAMLPERRC 240
Db 181 DVLYSSGTLHCPDQPSWVGCKSLVFLQVCIMANFFWLLVEGLYLHTLLVAMLPERRC 240

Qy 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIIIVNFVLF 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIIIVNFVLF 300

Qy 301 SIIRILLQKLTSPDVGNDQSOYKRLAKSTLLIPLFGVHYWVFAVPFISISKYQILFE 360
Db 301 SIIRILLQKLTSPDVGNDQSOYKRLAKSTLLIPLFGVHYWVFAVPFISISKYQILFE 360

Qy 361 LCLGSFQGLVVAVLYCFNLSEVQCELKRWKRSRCPGPSASRDYRVCGSSFRNGSEGAQ 420
Db 361 LCLGSFQGLVVAVLYCFNLSEVQCELKRWKRSRCPGPSASRDYRVCGSSFRNGSEGAQ 420

Qy 421 FHRGSRAGSFLQTETSVI 438
Db 421 FHRGSRAGSFLQTETSVI 438

RESULT 10
US-60-453-050-10294
; Sequence 10294, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001457
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10294
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-10294

Query Match      100.0%; Score 2342; DB 33; Length 438;
Best Local Similarity 100.0%; Pred. No. 1e-212;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60

Qy 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDVPDAGYSDPEDESKI 120
Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDVPDAGYSDPEDESKI 120
```

Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120
 Qy 121 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRYNIHLNLFSLFILRAISVLVKD 180
 Db 121 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRYNIHLNLFSLFILRAISVLVKD 180
 Qy 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYICIMANFFWLLVEGLYHHTLLVAMLPFPRRC 240
 Db 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYICIMANFFWLLVEGLYHHTLLVAMLPFPRRC 240
 Qy 241 FLAYLLIGWGLPTVCIGAWTAARLYEDTGCWDTNDHSPVWVIRIPILISIVNFVLF 300
 Db 241 FLAYLLIGWGLPTVCIGAWTAARLYEDTGCWDTNDHSPVWVIRIPILISIVNFVLF 300
 Qy 301 SIIRILLOKLTSPDVGGNDOSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILPE 360
 Db 301 SIIRILLOKLTSPDVGGNDOSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILPE 360
 Qy 361 LCLGSFQGLVAVLYCFNLSEVQCELCRKRWSRCPTPSASRDYRVCGSFSRNGSEGLQ 420
 Db 361 LCLGSFQGLVAVLYCFNLSEVQCELCRKRWSRCPTPSASRDYRVCGSFSRNGSEGLQ 420
 Qy 421 FHRGSRQSFLOTETSVI 438
 Db 421 FHRGSRQSFLOTETSVI 438

RESULT 11

US-60-453-135-10294
 ; Sequence 10294, Application US/60453135
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: IAKOUBOVA, Olga
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001456
 ; CURRENT APPLICATION NUMBER: US/60/453,135
 ; CURRENT FILING DATE: 2003-03-10
 ; NUMBER OF SEQ ID NOS: 82762
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10294
 ; LENGTH: 438
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-60-453-135-10294

Query Match 100.0%; Score 2342; DB 33; Length 438;
 Best Local Similarity 100.0%; Pred. No. 1e-212;
 Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIOEETKCAELLRSQTEKHKACSGVMDNIT 60
 Db 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIOEETKCAELLRSQTEKHKACSGVMDNIT 60

Qy 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120
 Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120

Qy 121 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRYNIHLNLFSLFILRAISVLVKD 180
 Db 121 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRYNIHLNLFSLFILRAISVLVKD 180

Qy 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYICIMANFFWLLVEGLYHHTLLVAMLPFPRRC 240
 Db 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYICIMANFFWLLVEGLYHHTLLVAMLPFPRRC 240

Qy 241 FLAYLLIGWGLPTVCIGAWTAARLYEDTGCWDTNDHSPVWVIRIPILISIVNFVLF 300
 Db 241 FLAYLLIGWGLPTVCIGAWTAARLYEDTGCWDTNDHSPVWVIRIPILISIVNFVLF 300

Qy 301 SIIRILLOKLTSPDVGGNDOSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILPE 360
 Db 301 SIIRILLOKLTSPDVGGNDOSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILPE 360

Qy 421 FHRGSRQSFLOTETSVI 438
 Db 421 FHRGSRQSFLOTETSVI 438

RESULT 13

US-60-465-241-5513
 ; Sequence 5513, Application US/60465241
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: BEGOVICH, Ann
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

Qy 361 LCLGSFQGLVAVLYCFNLSEVQCELCRKRWSRCPTPSASRDYRVCGSFSRNGSEGLQ 420
 Db 361 LCLGSFQGLVAVLYCFNLSEVQCELCRKRWSRCPTPSASRDYRVCGSFSRNGSEGLQ 420
 Qy 421 FHRGSRQSFLOTETSVI 438
 Db 421 FHRGSRQSFLOTETSVI 438

RESULT 12
 US-60-455-444-5513
 ; Sequence 5513, Application US/60455444
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: BEGOVICH, Ann
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001455
 ; CURRENT APPLICATION NUMBER: US/60/455,444
 ; CURRENT FILING DATE: 2003-03-18
 ; NUMBER OF SEQ ID NOS: 50986
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5513
 ; LENGTH: 438
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-60-455-444-5513

Query Match 100.0%; Score 2342; DB 33; Length 438;
 Best Local Similarity 100.0%; Pred. No. 1e-212;
 Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIOEETKCAELLRSQTEKHKACSGVMDNIT 60
 Db 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIOEETKCAELLRSQTEKHKACSGVMDNIT 60

Qy 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120
 Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120

Qy 121 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRYNIHLNLFSLFILRAISVLVKD 180
 Db 121 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRYNIHLNLFSLFILRAISVLVKD 180

Qy 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYICIMANFFWLLVEGLYHHTLLVAMLPFPRRC 240
 Db 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYICIMANFFWLLVEGLYHHTLLVAMLPFPRRC 240

Qy 241 FLAYLLIGWGLPTVCIGAWTAARLYEDTGCWDTNDHSPVWVIRIPILISIVNFVLF 300
 Db 241 FLAYLLIGWGLPTVCIGAWTAARLYEDTGCWDTNDHSPVWVIRIPILISIVNFVLF 300

Qy 301 SIIRILLOKLTSPDVGGNDOSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILPE 360
 Db 301 SIIRILLOKLTSPDVGGNDOSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILPE 360

Qy 361 LCLGSFQGLVAVLYCFNLSEVQCELCRKRWSRCPTPSASRDYRVCGSFSRNGSEGLQ 420
 Db 361 LCLGSFQGLVAVLYCFNLSEVQCELCRKRWSRCPTPSASRDYRVCGSFSRNGSEGLQ 420

Qy 421 FHRGSRQSFLOTETSVI 438
 Db 421 FHRGSRQSFLOTETSVI 438

; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001468
 ; CURRENT APPLICATION NUMBER: US/60/465,241
 ; CURRENT FILING DATE: 2003-04-23
 ; NUMBER OF SEQ ID NOS: 258418
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5513
 ; LENGTH: 438
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-60-465-241-5513

Query Match 100.0%; Score 2342; DB 33; Length 438;
 Best Local Similarity 100.0%; Pred. No. 1e-212;
 Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGWMDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGWMDNIT 60
QY 61 CWRPANVGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGSDPEDSKI 120
Db 61 CWRPANVGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGSDPEDSKI 120
QY 121 TFYLKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180
Db 121 TFYLKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180
QY 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240
Db 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300
QY 301 SIIRILLOKLTSPDVGGNDQSOYKRLAKSTLLIPLFGVHYVMFAVFPISISSKYQILFE 360
Db 301 SIIRILLOKLTSPDVGGNDQSOYKRLAKSTLLIPLFGVHYVMFAVFPISISSKYQILFE 360
QY 361 LCLGSFQGLVVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGAQ 420
Db 361 LCLGSFQGLVVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGAQ 420
QY 421 FHRGSAQSFIQTETSVI 438
Db 421 FHRGSAQSFIQTETSVI 438
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300
QY 301 SIIRILLOKLTSPDVGGNDQSOYKRLAKSTLLIPLFGVHYVMFAVFPISISSKYQILFE 360
Db 301 SIIRILLOKLTSPDVGGNDQSOYKRLAKSTLLIPLFGVHYVMFAVFPISISSKYQILFE 360
QY 361 LCLGSFQGLVVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGAQ 420
Db 361 LCLGSFQGLVVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGAQ 420
QY 421 FHRGSAQSFIQTETSVI 438
Db 421 FHRGSAQSFIQTETSVI 438

```

RESULT 14
 US-60-466-412-10294
 ; Sequence 10294, Application US/60466412
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: IAKOUROVA, Olga
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001466
 ; CURRENT APPLICATION NUMBER: US/60/466,412
 ; CURRENT FILING DATE: 2003-04-30
 ; NUMBER OF SEQ ID NOS: 429241
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10294
 ; LENGTH: 438
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-60-466-412-10294

Query Match 100.0%; Score 2342; DB 33; Length 438;
 Best Local Similarity 100.0%; Pred. No. 1e-212;
 Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGWMDNIT 60

```

```

Db 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGWMDNIT 60
QY 61 CWRPANVGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGSDPEDSKI 120
Db 61 CWRPANVGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGSDPEDSKI 120
QY 121 TFYLKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180
Db 121 TFYLKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180
QY 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240
Db 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300
QY 301 SIIRILLOKLTSPDVGGNDQSOYKRLAKSTLLIPLFGVHYVMFAVFPISISSKYQILFE 360
Db 301 SIIRILLOKLTSPDVGGNDQSOYKRLAKSTLLIPLFGVHYVMFAVFPISISSKYQILFE 360
QY 361 LCLGSFQGLVVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGAQ 420
Db 361 LCLGSFQGLVVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGAQ 420
QY 421 FHRGSAQSFIQTETSVI 438
Db 421 FHRGSAQSFIQTETSVI 438

```

RESULT 15

US-60-500-315-1460
 ; Sequence 1460, Application US/60500315
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
 ; TITLE OF INVENTION: ENCODING HUMAN G-PROTEIN COUPLED RECEPTOR PROTEINS, METHODS
 ; TITLE OF INVENTION: OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001484
 ; CURRENT APPLICATION NUMBER: US/60/500,315
 ; CURRENT FILING DATE: 2003-09-05
 ; NUMBER OF SEQ ID NOS: 69978
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1460
 ; LENGTH: 438
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-60-500-315-1460

Query Match 100.0%; Score 2342; DB 33; Length 438;
 Best Local Similarity 100.0%; Pred. No. 1e-212;
 Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGWMDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGWMDNIT 60
QY 61 CWRPANVGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGSDPEDSKI 120
Db 61 CWRPANVGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGSDPEDSKI 120
QY 121 TFYLKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180
Db 121 TFYLKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180
QY 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240
Db 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300

```

Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGWDNDHSVPWWVIRIPILISIIIVNFVLEI 300
Qy 301 SIIRILLQKLTSPDYGGNDQSOYKRIAKSTLLIIPFGVHYMVFAVFPISISSKYQIILFE 360
Db 301 SIIRILLQKLTSPDYGGNDQSOYKRIAKSTLLIIPFGVHYMVFAVFPISISSKYQIILFE 360
Qy 361 LCLGSFQGLVAVLYCFNLNSEQCELKKWRRCPTPSASRDYRVCGSFSRNGSEGALQ 420
Db 361 LCLGSFQGLVAVLYCFNLNSEQCELKKWRRCPTPSASRDYRVCGSFSRNGSEGALQ 420
Qy 421 FHRGSRQSFLOTETSVI 438
Db 421 FHRGSRQSFLOTETSVI 438

Search completed: June 22, 2004, 09:03:25
Job time : 185 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 22, 2004, 08:58:09 ; Search time 21 seconds
(without alignments)
950.959 Million cell updates/sec

Title: US-09-983-000A-20
Perfect score: 2342
Sequence: 1 MRTLPPALLTCWLLAPVNS.....LQFHGRSAQSFLOTETSVI 438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 302192 seqs, 45593913 residues

Total number of hits satisfying chosen parameters: 302192

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2342	100.0	438	6	US-10-831-393-10
2	2331	99.5	438	6	US-10-831-393-12
3	2327	99.4	438	6	US-10-831-393-11
4	2032	86.8	437	6	US-10-831-393-14
5	2032	86.8	437	6	US-10-831-393-16
6	2030	86.7	437	6	US-10-831-393-13
7	2020	86.3	437	6	US-10-831-393-15
8	1141.5	48.7	444	6	US-10-831-393-6
9	1086	46.5	459	6	US-10-831-393-3
10	1064.5	45.5	459	6	US-10-831-393-4
11	1064.5	45.5	459	6	US-10-831-393-8
12	1059	45.2	458	6	US-10-831-393-5
13	1059	45.2	458	6	US-10-831-393-7
14	1035.5	44.2	457	6	US-10-831-393-1
15	1035.5	44.2	457	7	US-60-568-073-1217
16	1026	43.8	447	6	US-10-831-393-9
17	1024	43.7	460	6	US-10-831-393-2
18	914.5	39.0	404	1	PCT-US04-09049-1
19	669	28.6	466	6	US-10-775-204-2219
20	669	28.6	466	6	US-10-796-307-662
21	669	28.6	466	7	US-60-550-051-292
22	644.5	27.5	419	6	US-10-796-307-663
23	644.5	27.5	419	7	US-60-550-051-293
24	564	24.1	443	1	PCT-US04-09049-10
25	486	20.8	411	6	US-10-821-502-8
26	483	20.6	431	6	US-10-821-502-2

27	482	20.6	411	6	US-10-821-502-4	Sequence 4, Appli
28	459.5	19.6	241	1	PCT-US04-09049-2	Sequence 2, Appli
29	451.5	19.3	504	6	US-10-489-425-32	Sequence 32, Appl
30	441.5	18.9	463	6	US-10-490-594-14	Sequence 14, Appl
31	434.5	18.6	464	6	US-10-490-594-12	Sequence 12, Appl
32	428.5	18.3	461	6	US-10-490-594-10	Sequence 10, Appl
33	424.5	18.1	431	6	US-10-489-425-30	Sequence 30, Appl
34	403.5	17.2	395	6	US-10-489-425-108	Sequence 108, App
35	224	9.6	618	6	US-10-473-391-7	Sequence 7, Appli
36	222	9.5	785	6	US-10-821-234-1164	Sequence 1164, Ap
37	222	9.5	835	1	PCT-US03-15011-56	Sequence 56, Appl
38	222	9.5	835	1	PCT-US03-15011-57	Sequence 57, Appl
39	219	9.4	823	1	PCT-US03-15011-44	Sequence 44, Appl
40	219	9.4	823	1	PCT-US03-15011-62	Sequence 62, Appl
41	217.5	9.3	872	1	PCT-US03-15011-66	Sequence 66, Appl
42	213.5	9.1	741	6	US-10-667-762-40	Sequence 40, Appl
43	210.5	9.0	344	1	PCT-US03-15011-63	Sequence 63, Appl
44	207	8.8	652	1	PCT-US03-15011-65	Sequence 65, Appl
45	207	8.8	652	6	US-10-667-762-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-831-393-10
; Sequence 10, Application US/10831393
; GENERAL INFORMATION:
; APPLICANT: Isfort, Robert
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F
; FILE REFERENCE: 8311
; CURRENT APPLICATION NUMBER: US/10/831,393
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US/09/694,519
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 438
; TYPE: PRT
; ORGANISM: homo sapiens;
US-10-831-393-10

Query Match	100.0%;	Score 2342;	DB 6;	Length 438;
Best Local Similarity	100.0%;	Pred. No. 1.1e-193;		
Matches	438;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MRTLPPALLTCWLLAPVNSIHPECRPHLEIQBEETKCAELLRSQTEKHKACSGWDNIT	60	
Db	1	MRTLPPALLTCWLLAPVNSIHPECRPHLEIQBEETKCAELLRSQTEKHKACSGWDNIT	60	
Qy	61	CWRPNYGETVTPCPKVFNFYSKAGNISKNCTSDGWSSTFPDFVACGYSDPEDESKI	120	
Db	61	CWRPNYGETVTPCPKVFNFYSKAGNISKNCTSDGWSSTFPDFVACGYSDPEDESKI	120	
Qy	121	TFYLKVAIYTLGVSVSLMSLATGSIILCLFRKLCHTRNYHNLFLSFILRAISVLKD	180	
Db	121	TFYLKVAIYTLGVSVSLMSLATGSIILCLFRKLCHTRNYHNLFLSFILRAISVLKD	180	
Qy	181	DVLYSSGTLHCPDQPSWGWCKLSLVFLOYCIMANFFWLLVEGLYHTLLVAMLPERRC	240	
Db	181	DVLYSSGTLHCPDQPSWGWCKLSLVFLOYCIMANFFWLLVEGLYHTLLVAMLPERRC	240	
Qy	241	FLAYLLIGWGLPTVCIGAWTAARLYEDTCGWDNDHNSVPMWVIRIPILISIIIVNVLFI	300	
Db	241	FLAYLLIGWGLPTVCIGAWTAARLYEDTCGWDNDHNSVPMWVIRIPILISIIIVNVLFI	300	
Qy	301	SIIRILLOKLTSPDVGNDOSQYKRLAKSTLLIPLFGVHYMVFAPVPISSKYQILFE	360	
Db	301	SIIRILLOKLTSPDVGNDOSQYKRLAKSTLLIPLFGVHYMVFAPVPISSKYQILFE	360	

QY 361 LCLGSFQGLVAVLYCFLNSELVQCELRKRWRCPTPSASRDYRVCGSSFSRNGSEGALQ 420
Db 361 LCLGSFQGLVAVLYCFLNSELVQCELRKRWRCPTPSASRDYRVCGSSFSRNGSEGALQ 420
QY 421 FHRGSAQSFLOTETSVI 438
Db 421 FHRGSAQSFLOTETSVI 438

RESULT 2
US-10-831-393-12
; Sequence 12, Application US/10831393
; GENERAL INFORMATION:
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors
; FILE REFERENCE: 8311
; CURRENT APPLICATION NUMBER: US/10/831,393
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US/09/694,519
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 12
; LENGTH: 438
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-831-393-12

Query Match 99.5%; Score 2331; DB 6; Length 438;
Best Local Similarity 99.5%; Pred. No. 9.6e-193;
Matches 436; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIQEETKCAELRSQTEKHKACSGVDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIQEETKCAELRSQTEKHKACSGVDNIT 60
QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETPPDFVDACGYSDPDESKI 120
Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETPPDFVDACGYSDPDESKI 120
QY 121 TFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRYNIHLNPLSLRAISVLVKD 180
Db 121 TFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRYNIHLNPLSLRAISVLVKD 180
QY 181 DVLYSSTGTLHCPDPSSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240
Db 181 DVLYSSTGTLHCPDPSSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIIIVNVLFI 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIIIVNVLFI 300
QY 301 SIIRILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYVMVFAVFPISISSKYQILFE 360
Db 301 SIIRILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYVMVFAVFPISISSKYQILFE 360
QY 361 LCLGSFQGLVAVLYCFLNSELVQCELRKRWRCPTPSASRDYRVCGSSFSRNGSEGALQ 420
Db 361 LCLGSFQGLVAVLYCFLNSELVQCELRKRWRCPTPSASRDYRVCGSSFSRNGSEGALQ 420
QY 421 FHRGSAQSFLOTETSVI 438
Db 421 FHRGSAQSFLOTETSVI 438

RESULT 3
US-10-831-393-11
; Sequence 11, Application US/10831393
; GENERAL INFORMATION:
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell

; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors
; FILE REFERENCE: 8311
; CURRENT APPLICATION NUMBER: US/10/831,393
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US/09/694,519
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 11
; LENGTH: 438
; TYPE: PRT
; ORGANISM: homo sapiens;
US-10-831-393-11

Query Match 99.4%; Score 2327; DB 6; Length 438;
Best Local Similarity 99.3%; Pred. No. 2.1e-192;
Matches 435; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIQEETKCAELRSQTEKHKACSGVDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIQEETKCAELRSQTEKHKACSGVDNIT 60
QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETPPDFVDACGYSDPDESKI 120
Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETPPDFVDACGYSDPDESKI 120
QY 121 TFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRYNIHLNPLSLRAISVLVKD 180
Db 121 TFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRYNIHLNPLSLRAISVLVKD 180
QY 181 DVLYSSTGTLHCPDPSSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240
Db 181 DVLYSSTGTLHCPDPSSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIIIVNVLFI 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIIIVNVLFI 300
QY 301 SIIRILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYVMVFAVFPISISSKYQILFE 360
Db 301 SIIRILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYVMVFAVFPISISSKYQILFE 360
QY 361 LCLGSFQGLVAVLYCFLNSELVQCELRKRWRCPTPSASRDYRVCGSSFSRNGSEGALQ 420
Db 361 LCLGSFQGLVAVLYCFLNSELVQCELRKRWRCPTPSASRDYRVCGSSFSRNGSEGALQ 420
QY 421 FHRGSAQSFLOTETSVI 438
Db 421 FHRGSAQSFLOTETSVI 438

RESULT 4
US-10-831-393-14
; Sequence 14, Application US/10831393
; GENERAL INFORMATION:
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors
; FILE REFERENCE: 8311
; CURRENT APPLICATION NUMBER: US/10/831,393
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US/09/694,519
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 14
; LENGTH: 437
; TYPE: PRT
; ORGANISM: rattus norvegicus;
US-10-831-393-14

Query Match 86.8%; Score 2032; DB 6; Length 437;
Best Local Similarity 87.4%; Pred. No. 5e-167;
Matches 373; Conservative 21; Mismatches 33; Indels 0; Gaps 0;

Qy 12 CWWLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGVMDNITCWRPANVGTV 71
Db 11 CWWLVRVSSIHPECRFHEIQEETKCAELLSSQWENHRACSGVMDNITCWRPADIGTV 70

Qy 72 TVPCPKVFSNFYSKAGNISKNCTSDGWSSETPDPFDVACGYSDPDESKITFYILVKAITY 131
Db 71 TVPCPKVFSNFYSRPGNISKNCTSDGWSSETPDPFDVACGYNDPDESKITFYILVKAITY 130

Qy 132 LGYSVSLMSLTGSIILCLFRKLHCTRYNIHLNLFSLFMRALSVLVKDVLYSSSGTLH 191
Db 131 LGYSVSLMSLTGSIILCLFRKLHCTRYNIHLNLFSLFMRALSVLVKDVLYSSSGTLR 190

Qy 192 CPDQPSWVGCKLSLVFQYICIMANFWLLVEGLYHTLLVAMLPFRRCFLAYLLIGWL 251
Db 191 CHDQPSWVGCKLSLVFQYICIMANFWLLVEGLYHTLLVAILPPSRCLFAYLLIGWI 250

Qy 252 PTVCIGAWTAARLYLEDTGCDTNDHSPWVIRIPILISIVNFVLFISIRILLQKLT 311
Db 251 PSVCIGAWIATRLSLEDTGCDTNDHSPWVIRIPILISIVNFALFISIRILLQKLT 310

Qy 312 SPDVGGNDQSQYKRLAKSTLLIPFGVHYMVFAVFPISISSKYQIILFELCLGSFQGLV 371
Db 311 SPDVGGNDQSQYKRLAKSTLLIPFGVHYMVFAAFPIGISTYQIILFELCVGSFQGLV 370

Qy 372 AVLYCFNLSEVQCELKRWKRCPTPSASRDYRVCGSFSRNGSEGALQHRGSRASFL 431
Db 371 AVLYCFNLSEVQCELKRWGRCLTQPSGRDYRLHWSMRSNGSESALQHRGSRTOSEL 430

Qy 432 QTETSVI 438
Db 431 QSETSUI 437

RESULT 5
US-10-831-393-16
; Sequence 16, Application US/10831393
; GENERAL INFORMATION:
; APPLICANT: Isfort, Robert
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or H
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors
; FILE REFERENCE: 8311
; CURRENT APPLICATION NUMBER: US/10/831,393
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US/09/694,519
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 437
; TYPE: PRT
; ORGANISM: rat;
US-10-831-393-16

Query Match 86.8%; Score 2032; DB 6; Length 437;
Best Local Similarity 87.4%; Pred. No. 5e-167;
Matches 373; Conservative 21; Mismatches 33; Indels 0; Gaps 0;

Qy 12 CWWLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGVMDNITCWRPANVGTV 71
Db 11 CWWLVRVSSIHPECRFHEIQEETKCAELLSSQWENHRACSGVMDNITCWRPADIGTV 70

Qy 72 TVPCPKVFSNFYSKAGNISKNCTSDGWSSETPDPFDVACGYSDPDESKITFYILVKAITY 131
Db 71 TVPCPKVFSNFYSRPGNISKNCTSDGWSSETPDPFDVACGYNDPDESKITFYILVKAITY 130

Qy 132 LGYSVSLMSLTGSIILCLFRKLHCTRYNIHLNLFSLFMRALSVLVKDVLYSSSGTLH 191
Db 131 LGYSVSLMSLTGSIILCLFRKLHCTRYNIHLNLFSLFMRALSVLVKDVLYSSSGTLR 190

Qy 192 CPDQPSWVGCKLSLVFQYICIMANFWLLVEGLYHTLLVAMLPFRRCFLAYLLIGWL 251
Db 191 CHDQPSWVGCKLSLVFQYICIMANFWLLVEGLYHTLLVAILPPSRCLFAYLLIGWI 250

Qy 252 PTVCIGAWTAARLYLEDTGCDTNDHSPWVIRIPILISIVNFVLFISIRILLQKLT 311
Db 251 PSVCIGAWIATRLSLEDTGCDTNDHSPWVIRIPILISIVNFALFISIRILLQKLT 310

Qy 312 SPDVGGNDQSQYKRLAKSTLLIPFGVHYMVFAVFPISISSKYQIILFELCLGSFQGLV 371
Db 311 SPDVGGNDQSQYKRLAKSTLLIPFGVHYMVFAAFPIGISTYQIILFELCVGSFQGLV 370

Qy 372 AVLYCFNLSEVQCELKRWKRCPTPSASRDYRVCGSFSRNGSEGALQHRGSRASFL 431
Db 371 AVLYCFNLSEVQCELKRWGRCLTQPSGRDYRLHWSMRSNGSESALQHRGSRTOSEL 430

Qy 432 QTETSUI 438
Db 431 QSETSUI 437

RESULT 6
US-10-831-393-13
; Sequence 13, Application US/10831393
; GENERAL INFORMATION:
; APPLICANT: Isfort, Robert
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or I
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors
; FILE REFERENCE: 8311
; CURRENT APPLICATION NUMBER: US/10/831,393
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US/09/694,519
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 437
; TYPE: PRT
; ORGANISM: mus musculus;
US-10-831-393-13

Query Match 86.7%; Score 2030; DB 6; Length 437;
Best Local Similarity 87.4%; Pred. No. 7.5e-167;
Matches 373; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

Qy 12 CWWLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGVMDNITCWRPANVGTV 71
Db 11 CWWLVRVSSIHPECRFHEIQEETKCAELLSSQWENHRACSGVMDNITCWRPADVGTV 70

Qy 72 TVPCPKVFSNFYSKAGNISKNCTSDGWSSETPDPFDVACGYSDPDESKITFYILVKAITY 131
Db 71 TVPCPKVFSNFYSRPGNISKNCTSDGWSSETPDPFDVACGYNDPDESKISFYILVKAITY 130

Qy 132 LGYSVSLMSLTGSIILCLFRKLHCTRYNIHLNLFSLFMRALSVLVKDVLYSSSGTLH 191
Db 131 LGYSVSLMSLTGSIILCLFRKLHCTRYNIHLNLFSLFMRALSVLVKDVLYSSSGTLR 190

Qy 192 CPDQPSWVGCKLSLVFQYICIMANFWLLVEGLYHTLLVAMLPFRRCFLAYLLIGWL 251
Db 191 CHDQPSWVGCKLSLVFQYICIMANFWLLVEGLYHTLLVAILPPSRCLFAYLLIGWI 250

Qy 252 PTVCIGAWTAARLYLEDTGCDTNDHSPWVIRIPILISIVNFVLFISIRILLQKLT 311
Db 251 PSVCIGAWIATRLSLEDTGCDTNDHSPWVIRIPILISIVNFALFISIRILLQKLT 310

Qy 312 SPDVGGNDQSQYKRLAKSTLLIPFGVHYMVFAVFPISISSKYQIILFELCLGSFQGLV 371
Db 311 SPDVGGNDQSQYKRLAKSTLLIPFGVHYMVFAAFPIGISTYQIILFELCVGSFQGLV 370

Qy 372 AVLYCFNLSEVQCELKRWKRCPTPSASRDYRVCGSFSRNGSEGALQHRGSRASFL 431
Db 371 AVLYCFNLSEVQCELKRWGRCLTQPSGRDYRLHWSMRSNGSESALQHRGSRTOSEL 430

Db 371 AVLYCFNLSEVOCELKRRWRGLCLTQAGSRDYRLHSWSMRNGSESGALQIHRGSRQSF 430
QY 432 QETSVI 438
Db 431 QETSVI 437

RESULT 7

US-10-831-393-15
; Sequence 15, Application US/10831393
; GENERAL INFORMATION:
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors
; FILE REFERENCE: 8311
; CURRENT APPLICATION NUMBER: US/10/831,393
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US/09/694,519
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 437
; TYPE: PRT
; ORGANISM: rattus norvegicus;
US-10-831-393-15

Query Match 86.3%; Score 2020; DB 6; Length 437;
Best Local Similarity 87.1%; Pred. No. 5.4e-166;
Matches 372; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 12 CWLLAPVNSIHPECRPHLEIQBEETKCAELLRSQTEKHKACSGVNDNITCWPNVGETV 71
Db 11 CWLLVRVSSIHPECRPHLEIQBEETKCAELLRSQTEKHKACSGVNDNITCWPNVGETV 70
QY 72 TVPCPKVFSNFYSKAGNISKNCTSDGSETFPDFVDACGSDPEDESKITFYILVKAITY 131
Db 71 TVPCPKVFSNFYSRPGNISKNCTSDGSETFPDFVDACGSDPEDESKITFYILVKAITY 130
QY 132 LGYSVLSMLATGSIILCLFRKLHCTRYNIHLNPLSFILRAISVLVKDDVLYSSGTLH 191
Db 131 LGYSVLSMLATGSIILCLFRKLHCTRYNIHLNPLSFILRAISVLVKDDVLYSSGTLR 190
QY 192 CPDPQSSWVGCKLSLVFLOYCIMANFFWLLVEGLYLHTLLVAMLPKRCFLAYLLIGWL 251
Db 191 CHDQGSWVGCKLSLVFLOYCIMANFFWLLVEGLYLHTLLVAMLPKRCFLAYLLIGWI 250
QY 252 PVVTCGAWTAARLYLEDTCGWDNDHNSVPMWVIRIPILISIVNFWLFTSIRILLQKLT 311
Db 251 PSVCIGAWTATLSLEDTCGWDNDHNSIPMWVIRIPILISIVNFWLFTSIRILLQKLT 310
QY 312 SPDVGNDQSOYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQLLFELCLGSGQGLVV 371
Db 311 SPDVGNDQSOYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQLLFELCLGSGQGLVV 370
QY 372 AVLYCFNLSEVOCELKRRWRSCPTPSASRDYRVCGSFRNGSESGALQIHRGSRQSF 431
Db 371 AVLYCFNLSEVOCELKRRWRGLCLTQAGSRDYRLHSWSMRNGSESGALQIHRGSRQSF 430
QY 432 QETSVI 438
Db 431 QETSVI 437

RESULT 8

US-10-831-393-6
; Sequence 6, Application US/10831393
; GENERAL INFORMATION:
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors

; FILE REFERENCE: 8311
; CURRENT APPLICATION NUMBER: US/10/831,393
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US/09/694,519
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: rana ridibunda;
US-10-831-393-6

Query Match 48.7%; Score 1141.5; DB 6; Length 444;
Best Local Similarity 51.9%; Pred. No. 2e-90;
Matches 233; Conservative 65; Mismatches 128; Indels 23; Gaps 10;

QY 5 LPPALLTCWLLAPVNSIHPEC--RPHLEIQBEETKCAELLRSQTEKHKACSGVNDNITCW 62
Db 4 LPLLCLCLTGLSPILCVPEECSIMYQIELKHEECVNHEDYFNDT---AVCKRTWNNITCW 60
QY 63 RPANVGETVTVPCPKVFSNFYSKA--GNISKNCTSDGSETFP--DFVDACGYS--DPDE 117
Db 61 PSASIGEVVVLQCPGYFSMFTTGTVNGVSNKCTSEGWSMYPATYAAACGFSNDTPTPE 120
QY 118 SKITFYILVKAITYLGYSVLSMLATGSIILCLFRKLHCTRYNIHLNPLSFILRAISVL 177
Db 121 QTVFEGAIGTYTIGHLSLSLTAAMLIILCIPFKLHCTRYNIHMLFMSFIMRAIAVF 180
QY 178 VKDDVLYSSGTLHCPDQSPSSWVGCKLSLVFLOYCIMANFFWLLVEGLYLHTLLV-AMLP 236
Db 181 IKDVLVFSGESDHC--HVGSVGCAAMVFOYICIMANFFWLLVEGLYLHNLVISPFS 237
QY 237 PRRCFLAYLLIGWLPTVCIGAWTAARLYLEDTCGWDNDHNSVPMWVIRIPILISIVNF 296
Db 238 EKKYFWWVILIGWGAAPSVEFITAWSLARVYFEDTGCWDTIESHL-WWIKTPIVLSILVNF 296
QY 297 VLFISIRILLQKLTSPDVGNDQSOYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQ 356
Db 297 ILFICIRILLVQKLSHPDVGNENSQYTRLAKSTLLIPLFGVHYMFAFPDNPKEVK 356
QY 357 ILFELCLGSGQGLVVAVLYCFNLSEVOCELKRRWRSCPTPSASRDYRVCGSFRNGSE 416
Db 357 LVFELILGSGQGLVVAVLYCFNLSEVOCELKRRWRNLERFMGKMKYVHPSLGSNGTN 416
QY 417 GALQFH-----RGSRAQSFLQETSVI 438
Db 417 FSTQISMLTKCSPKTRRCSSF-QAEFSILV 444

RESULT 9

US-10-831-393-4
; Sequence 4, Application US/10831393
; GENERAL INFORMATION:
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors
; FILE REFERENCE: 8311
; CURRENT APPLICATION NUMBER: US/10/831,393
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US/09/694,519
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 459
; TYPE: PRT
; ORGANISM: mus musculus;
US-10-831-393-4

Query Match 46.4%; Score 1086; DB 6; Length 459;
Best Local Similarity 48.5%; Pred. No. 1.3e-85;

Matches 225; Conservative 67; Mismatches 132; Indels 40; Gaps 11;

Qy 5 LPPALLTCWL-----LAPVN-----SHPECRFHELETOEBETKCAELLSQTE-KHKAC 52
Db 6 LPPARWLCLVALACALGPAGSRAAPHQCEYLQMIKORQOCLE--EAQLENKTTGC 63
Qy 53 SGVWDNITCWRPANVGETVTPCPKVFNSFYKAG-NISKCTSDGMSSETPP-DFVDACG 110
Db 64 SKMWDNLTCWPTTPWGQVVDLDCPLIQLFSPHGYNISRNCTEGWSQLEPGFYHACG 123
Qy 111 YSD-----PEDESKITFYILVKAIYTLGYSVLSMLATGSIILCLPRKLHCTRNVIHNLFP 166
Db 124 LNDRASSMDEQOQTEFYDAVKTGTIGYSLASLLVAMAILSLFRKLHCTRNVIHMLF 183
Qy 167 LSFILRAISLVKDDVLYSSGTLHCPDQPSWSWGCKLSLVFLQYCIANFVFWLLVGLY 226
Db 184 MSFILRATAVFIKQMAFNGETDHCSE---ASVCKAAVVFQYCVMANFVFWLLVGLY 240
Qy 227 LHTLL-VAMLPFRRCFLAYLLIGWGLTVCIGAWTAARLYLEDTCGWDTHDHSVPMVIR 285
Db 241 LHTLLAVSFPSERKVFVGYILLGWGVPFVIMTIVIRIHFEDFGCWDTHINSSLWLIK 300
Qy 286 IPIILISIVNFVLSIRILLQKLTSPDVGNDSQYKRLAKSTLLIPLFGVHYWVFA 345
Db 301 GPILISILVNFILFICIRILVQKLRPPDIGNKNDSSPYSLAKSTLLIPLFGVHYWVFA 360
Qy 346 VFPISISSKYQLFELCLGSGFQGLVAVLYCFINSEVOCELKRWK-----SRC 394
Db 361 FFPDNFAQVKNVVELVVGSGFGFVVALYCFINSEVOCELKRWK-----SRC 420
Qy 395 PTPSASRDYRVCGSFRNGSEALQPHRGSRAQSFLOTETSVI 438
Db 421 QHPWGGSGNGVSCSTQVSM-----LTRVSPSARRSSSFQAEVSLV 459

RESULT 10
US-10-831-393-3
; Sequence 3, Application US/10831393
; GENERAL INFORMATION:
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors
; FILE REFERENCE: 8311
; CURRENT APPLICATION NUMBER: US/10/831.393
; PRIOR FILING DATE: 2004-04-23
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 3
; LENGTH: 459
; TYPE: PRT
; ORGANISM: rattus norvegicus;
US-10-831-393-3

Query Match 45.5%; Score 1064.5; DB 6; Length 459;
Best Local Similarity 47.1%; Pred. No. 8.9e-84;
Matches 221; Conservative 68; Mismatches 139; Indels 41; Gaps 11;

Qy 1 MRTLLPP-----ALLTCWLLAPVN-----SHPECRFHELETOEBETKCAELLSQTE 47
Db 1 MRPPSPPHVRLCWLVALAGALAC-ALRPAGSQAASPHQCEYLQLEIQRQOCLEBAQLENE 59
Qy 48 KHKACSGVWDNITCWRPANVGETVTPCPKVFNSFYKAG-NISKCTSDGMSSETPP-DF 105
Db 60 T-TCCSKWMDNLTCWPTTPRQAVVLDCLPLIFQIFAPIHGYNISRSCTEGWSQLEPGY 118
Qy 106 VDAGYSDP-----BDESKITFYILVKAIYTLGYSVLSMLATGSIILCLPRKLHCTRNVI 161
Db 119 HIACGLNDRASSLDEQOQTKFYNTVKTGTIGYSLASLLVAMAILSLFRKLHCTRNVI 178
Qy 162 HMLNLFILRAISLVKDDVLYSSGTLHCPDQPSWSWGCKLSLVFLQYCIANFVFWLL 221
Db 179 HMLNLFILRAISLVKDDVLYSSGTLHCPDQPSWSWGCKLSLVFLQYCIANFVFWLL 235
Qy 222 VEGLYLHTLL-VAMLPFRRCFLAYLLIGWGLTVCIGAWTAARLYLEDTCGWDTHDHSV 280
Db 236 VEGLYLHTLL-VAMLPFRRCFLAYLLIGWGLTVCIGAWTAARLYLEDTCGWDTHDHSV 295
Qy 281 WWIRIPILISIVNFVLSIRILLQKLTSPDVGNDSQYKRLAKSTLLIPLFGVH 340
Db 296 WWIKAPILISILVNFVLSIRILLQKLTSPDVGNDSQYKRLAKSTLLIPLFGVH 355
Qy 341 YMFVAVFPISISSKYQLFELCLGSGFQGLVAVLYCFINSEVOCELKRWK----- 391
Db 356 YMFVAVFPISISSKYQLFELCLGSGFQGLVAVLYCFINSEVOCELKRWK----- 415

Db 179 HMLNLFILRAISLVKDDVLYSSGTLHCPDQPSWSWGCKLSLVFLQYCIANFVFWLL 235
Qy 222 VEGLYLHTLL-VAMLPFRRCFLAYLLIGWGLTVCIGAWTAARLYLEDTCGWDTHDHSV 280
Db 236 VEGLYLHTLL-VAMLPFRRCFLAYLLIGWGLTVCIGAWTAARLYLEDTCGWDTHDHSV 295
Qy 281 WWIRIPILISIVNFVLSIRILLQKLTSPDVGNDSQYKRLAKSTLLIPLFGVH 340
Db 296 WWIKAPILISILVNFVLSIRILLQKLTSPDVGNDSQYKRLAKSTLLIPLFGVH 355
Qy 341 YMFVAVFPISISSKYQLFELCLGSGFQGLVAVLYCFINSEVOCELKRWK----- 391
Db 356 YMFVAVFPISISSKYQLFELCLGSGFQGLVAVLYCFINSEVOCELKRWK----- 415

RESULT 11
US-10-831-393-8
; Sequence 8, Application US/10831393
; GENERAL INFORMATION:
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or I
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors
; FILE REFERENCE: 8311
; CURRENT APPLICATION NUMBER: US/10/831.393
; PRIOR FILING DATE: 2004-04-23
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 8
; LENGTH: 459
; TYPE: PRT
; ORGANISM: rattus sp;
US-10-831-393-8

Query Match 45.5%; Score 1064.5; DB 6; Length 459;
Best Local Similarity 47.1%; Pred. No. 8.9e-84;
Matches 221; Conservative 68; Mismatches 139; Indels 41; Gaps 11;

Qy 1 MRTLLPP-----ALLTCWLLAPVN-----SHPECRFHELETOEBETKCAELLSQTE 47
Db 1 MRPPSPPHVRLCWLVALAGALAC-ALRPAGSQAASPHQCEYLQLEIQRQOCLEBAQLENE 59
Qy 48 KHKACSGVWDNITCWRPANVGETVTPCPKVFNSFYKAG-NISKCTSDGMSSETPP-DF 105
Db 60 T-TCCSKWMDNLTCWPTTPRQAVVLDCLPLIFQIFAPIHGYNISRSCTEGWSQLEPGY 118
Qy 106 VDAGYSDP-----BDESKITFYILVKAIYTLGYSVLSMLATGSIILCLPRKLHCTRNVI 161
Db 119 HIACGLNDRASSLDEQOQTKFYNTVKTGTIGYSLASLLVAMAILSLFRKLHCTRNVI 178
Qy 162 HMLNLFILRAISLVKDDVLYSSGTLHCPDQPSWSWGCKLSLVFLQYCIANFVFWLL 221
Db 179 HMLNLFILRAISLVKDDVLYSSGTLHCPDQPSWSWGCKLSLVFLQYCIANFVFWLL 235
Qy 222 VEGLYLHTLL-VAMLPFRRCFLAYLLIGWGLTVCIGAWTAARLYLEDTCGWDTHDHSV 280
Db 236 VEGLYLHTLL-VAMLPFRRCFLAYLLIGWGLTVCIGAWTAARLYLEDTCGWDTHDHSV 295
Qy 281 WWIRIPILISIVNFVLSIRILLQKLTSPDVGNDSQYKRLAKSTLLIPLFGVH 340
Db 296 WWIKAPILISILVNFVLSIRILLQKLTSPDVGNDSQYKRLAKSTLLIPLFGVH 355
Qy 341 YMFVAVFPISISSKYQLFELCLGSGFQGLVAVLYCFINSEVOCELKRWK----- 391
Db 356 YMFVAVFPISISSKYQLFELCLGSGFQGLVAVLYCFINSEVOCELKRWK----- 415

```

QY 392 --SRCPTPSASRDYRVCGSFSRNGSGALQFHRGSAQSFLQTETSVI 438
Db 416 WSSKSOHPWGSGNGATCSTQVSM-----LTRVSPSARRSSSFQAESLV 459

RESULT 12
US-10-831-393--5
; Sequence 5, Application US/10831393
; GENERAL INFORMATION:
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors
; FILE REFERENCE: 8311
; CURRENT APPLICATION NUMBER: US/10/831,393
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US/09/694,519
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 458
; TYPE: PRT
; ORGANISM: sus scrofa;
US-10-831-393--5

Query Match 45.2%; Score 1059; DB 6; Length 458;
Best Local Similarity 46.9%; Pred. No. 2.7e-83;
Matches 220; Conservative 65; Mismatches 142; Indels 42; Gaps 12;

QY 1 MRTLLPP-----ALLTCWLLAPVNS-----IHPECRFHLEIOBEETKCAELLRSQ 46
Db 1 MRPLSPPPAGFCVLAVGLAC-VLGPVGSWAVGLQEBCDYLQMIKVQHKKCLEEAQLN 59
QY 47 EKHKACSGVDNITCWEPANVGETVTVPCKVFNSFYSKAG-NISKNCSTDGSETFP-D 104
Db 60 ET-SGCSKMNDNLFCWPATPRGVVVILACPLIFKLFSPTQGLNVSRNCTDEGWTFLEPG 118
QY 105 FVDACGYSDPE---DESKIITYILVKAIYTLGYSVLSMLSATGSIIICLFERKLHCTRN 161
Db 119 YPIACGMDDKASGLDEQOQTVFNSVKTYGTIGYSLSAALLVATAILLSFRKLHCTRN 178
QY 162 HLNLEFILRAISVLVKDDVLVYSSSTGLHCPODPSSWGCCKLSLVLOVCIMANPFWLL 221
Db 179 HMHLFIILIRATAVFKIDALDFSESDHC---SKGSVGCKAAVWLFOCVMANPFWLL 235
QY 222 VEGLYLHTLL-VAMLPERRCFLAYLLICWGLTPTVICIGANTAARLYLEDTCGDNDHSVP 280
Db 236 VEGLYLHTLLAVSFFSERKYPFGWGFVGVGVPSTFINMTVTVRIHFEDYGWDI-IHSSL 294
QY 281 WWIIRIPILSIIVNFVLFISIIRILLIKLTSPDVGNDSOYKRLAKSTILLIPIFGVH 340
Db 295 WWIIRIPILSIIVNFVLFISIIRILLIKLTSPDVGNDSOYKRLAKSTILLIPIFGVH 354
QY 341 YMFVAVPPISSKYQILFELCLGSGOGLVAVLYCFINSEVOCELKRKKR----- 391
Db 355 YINFAPPDNFAEVKMWVELIYVSGFCVCVAILYCFINCEVAQLRKRRWHQQVGLG 414
QY 392 --SRCPTPSASRDYRVCGSFSRNGSGALQFHRGSAQSFLQTETSVI 438
Db 415 WDSKYQHPSPGSGNGDTGSTQVSM-----LTRVSPSARRSSSFQAESLV 458

RESULT 13
US-10-831-393-7
; Sequence 7, Application US/10831393
; GENERAL INFORMATION:
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors
; FILE REFERENCE: 8311
; CURRENT APPLICATION NUMBER: US/10/831,393

```

```
QY 1 MRTLTP-PALLTC-----WLLAPVNS-----IHPECRFHLEIOEBETKCAELLRSQTEK 48
Db 1 MRPPSPUPARWLCVLGALAWALGAGQAARLQEECDYVQMIEVQHVKQCLUEAQLENET 60
QY 49 HKACSGVNDNITCWRPANVGETVTVPCPKVPSNFYSKAG-NISKNTSDGMSFTFP-DFV 106
Db 61 -IGCSKMDNLTCPATPRGQVWVLAELPLIFKLFSIQGRNVSRSCDTDEGWTLEPGYP 119
QY 107 DACGYSDEPE---DESKITFYILVKAITYLTVGSVSLMSLATGSIILCLFRKLHCTRYIHL 163
Db 120 IACGLDDKAASLDEQQTWTFYGSVKTGYTIGVGLSLATALLVATALLSLFRKLHCTRYIHM 179
QY 164 NLFLSFILRAISVLVVKDDVLYSSSGLHCPDPQSPSWGCKLSLVFLQYCYMANFVLLIVE 223
Db 180 HLFISFILRAAAVFIKDALFDSGESDQCE---GSVGCKAAMVFFQYCVMANFVLLIVE 236
QY 224 GLYLHTLL-VAMLPERRCFLAYLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMW 282
Db 237 GLYLHTLLAVSFYFFSERKYFWGYIILIGWGPSTFTVMVWTIARIHFEDYGCWDTINSSL-WW 295
QY 283 VIRIPILISIIIVNFVLFIISIIRILLOKLTSPDVGNDSQYKRLAKSTLLIPLFGVHYM 342
Db 296 IIKGPILTSILVNFILFICIIRILLOKLRPPDIRKSDSPYSRLARSTLLIPLFGVHYI 355
QY 343 VFVFPISISKYQILFELCLGSPQGLVAVLYVLYCFLNSEVQCELRKRW----- 391
Db 356 MFAFEPDNFXDEKVMFELVVGSGFQVVAIYCFLNGEVQAEELRRKRWRLHQLGVLGWN 415
QY 392 SRCPTPSASRDYRVCGSFSRNGSEGAQOFRGSRASQFLQETSVI 438
Db 416 PKYRHPGGSGNGATCSTQVSM-----LTRVSPGARRSSSFQAEVSLV 457
```

RESULT 15

US-60-568-073-1217

; Sequence 1217, Application US/60568073

; GENERAL INFORMATION:

; APPLICANT: Huang, Fei

; APPLICANT: Han, Xia

; APPLICANT: Shaw, Peter

; APPLICANT: Clark, Edwin

; TITLE OF INVENTION: COLON CANCER BIOMARKERS

; FILE REFERENCE: 10205 PSP

; CURRENT APPLICATION NUMBER: US/60/568,073

; CURRENT FILING DATE: 2004-05-04

; NUMBER OF SEQ ID NOS: 1305

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1217

; LENGTH: 457

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-60-568-073-1217

```
Query Match 44.2%; Score 1035.5; DB 7; Length 457;
Best Local Similarity 46.3%; Pred No. 2.8e-81;
Matches 216; Conservative 68; Mismatches 144; Indels 39; Gaps 12;
```

```
QY 1 MRTLTP-PALLTC-----WLLAPVNS-----IHPECRFHLEIOEBETKCAELLRSQTEK 48
Db 1 MRPPSPUPARWLCVLGALAWALGAGQAARLQEECDYVQMIEVQHVKQCLUEAQLENET 60
QY 49 HKACSGVNDNITCWRPANVGETVTVPCPKVPSNFYSKAG-NISKNTSDGMSFTFP-DFV 106
Db 61 -IGCSKMDNLTCPATPRGQVWVLAELPLIFKLFSIQGRNVSRSCDTDEGWTLEPGYP 119
QY 107 DACGYSDEPE---DESKITFYILVKAITYLTVGSVSLMSLATGSIILCLFRKLHCTRYIHL 163
Db 120 IACGLDDKAASLDEQQTWTFYGSVKTGYTIGVGLSLATALLVATALLSLFRKLHCTRYIHM 179
QY 164 NLFLSFILRAISVLVVKDDVLYSSSGLHCPDPQSPSWGCKLSLVFLQYCYMANFVLLIVE 223
Db 180 HLFISFILRAAAVFIKDALFDSGESDQCE---GSVGCKAAMVFFQYCVMANFVLLIVE 236
```